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FIG. 1

```
GGATCCCTGCTCCAGCAGCTGCAAGGTGCAAGAAGAAGAAGATCCCAGGGAGGAAAATGTG    120
                                                        M  C        2
CTGGAGACCCCTGTGTCGGTTCCTGTGGCTTTGGTCCTATCTGTCTTATGTTCAAGCAGT    180
 W  R  P  L  C  R  F  L  W  L  W  S  Y  L  S  Y  V  Q  A  V      22
GCCTATCCAGAAAGTCCAGGATGACACCAAAACCCTCATCAAGACCATTGTCACCAGGAT    240
 P  I  Q  K  V  Q  D  D  T  K  T  L  I  K  T  I  V  T  R  I      42
CAATGACATTTCACACACGCAGTCGGTATCCGCCAAGCAGAGGGTCACTGGCTTGGACTT    300
 N  D  I  S  H  T  Q  S  V  S  A  K  Q  R  V  T  G  L  D  F      62
CATTCCTGGGCTTCACCCCATTCTGAGTTTGTCCAAGATGGACCAGACTCTGGCAGTCTA    360
 I  P  G  L  H  P  I  L  S  L  S  K  M  D  Q  T  L  A  V  Y      82
TCAACAGGTCCTCACCAGCCTGCCTTCCCAAAATGTGCTGCAGATAGCCAATGACCTGGA    420
 Q  Q  V  L  T  S  L  P  S  Q  N  V  L  Q  I  A  N  D  L  E     102
GAATCTCCGAGACCTCCTCCATCTGCTGGCCTTCTCCAAGAGCTGCTCCCTGCCTCAGAC    480
 N  L  R  D  L  L  H  L  L  A  F  S  K  S  C  S  L  P  Q  T     122
CAGTGGCCTGCAGAAGCCAGAGAGCCTGGATGGCGTCCTGGAAGCCTCACTCTACTCCAC    540
 S  G  L  Q  K  P  E  S  L  D  G  V  L  E  A  S  L  Y  S  T     142
AGAGGTGGTGGCTTTGAGCAGGCTGCAGGGCTCTCTGCAGGACATTCTTCAACAGTTGGA    600
 E  V  V  A  L  S  R  L  Q  G  S  L  Q  D  I  L  Q  Q  L  D     162
TGTTAGCCCTGAATGCTGAAGTTTCAAAGGCCACCAGGCTCCCAAGAATCATGTAGAGGG    660
 V  S  P  E  C  *                                              167
AAGAAACCTTGGCTTCCAGGGGTCTTCAGGAGAAGAGAGCCATGTGCACACATCCATCAT    720
TCATTTCTCTCCCTCCTGTAGACCACCCATCCAAAGGCATGACTCCACAATGCTTGACTC    780
AAGTTATCCACACAACTTCATGAGCACAAGGAGGGGCCAGCCTGCAGAGGGGACTCTCAC    840
CTAGTTCTTCAGCAAGTAGAGATAAGAGCCATCCCATCCCCTCCATGTCCCACCTGCTCC    900
GGGTACATGTTCCTCCGTGGGTACACGCTTCGCTGCGGCCCAGGAGAGGTGAGGTAGGGA    960
TGGGTAGAGCCTTTGGGCTGTCTCAGAGTCTTTGGGAGCACCGTGAAGGCTGCATCCACA   1020
CACAGCTGGAAACTCCCAAGCAGCACACGATGGAAGCACTTATTTATTTATTCTGCATTC   1080
TATTTTGGATGGATCTGAAGCAAGGCATCAGCTTTTTCAGGCTTTGGGGGTCAGCCAGGA   1140
TGAGGAAGGCTCCTGGGGTGCTGCTTTCAATCCTATTGATGGGTCTGCCCGAGGCAAACC   1200
TAATTTTTGAGTGACTGGAAGGAAGGTTGGGATCTTCCAAACAAGAGTCTATGCAGGTAG   1260
CGCTCAAGATTGACCTCTGGTGACTGGTTTTGTTTCTATTGTGACTGACTCTATCCAAAC   1320
ACGTTTGCAGCGGCATTGCCGGGAGCATAGGCTAGGTTATTATCAAAAGCAGATGAATTT   1380
TGTCAAGTGTAATATGTATCTATGTGCACCTGAGGGTAGAGGATGTGTTAGAGGGAGGGT   1440
GAAGGATCCGGAAGTGTTCTCTGAATTACATATGTGTGGTAGGCTTTTCTGAAAGGGTGA   1500
GGCATTTTCTTACCTCTGTGGCCACATAGTGTGGCTTTGTGAAAAGGACAAAGGAGTTGA   1560
CTCTTTCCGGAACATTTGGAGTGTACCAGGCACCCTTGGAGGGGCTAAAGCTACAGGCCT   1620
TTTGTTGGCATATTGCTGAGCTCAGGGAGTGAGGGCCCCACATTTGAGACAGTGAGCCCC   1680
AAGAAAAGGGTCCCTGGTGTAGATCTCCAAGGTTGTCCAGGGTTGATCTCACAATGCGTT   1740
TCTTAAGCAGGTAGACGTTTGCATGCCAATATGTGGTTCTCATCTGATTGGTTCATCCAA   1800
AGTAGAACCCTGTCTCCCACCCATTCTGTGGGGAGTTTTGTTCCAGTGGGAATGAGAAAT   1860
CACTTAGCAGATGGTCCTGAGCCCTGGGCCAGCACTGCTGAGGAAGTGCCAGGGCCCCAG   1920
GCCAGGCTGCCAGAATTGCCCTTCGGGCTGGAGGATGAACAAAGGGGCTTGGGTTTTTCC   1980
ATCACCCCTGCACCCTATGTCACCATCAAACTGGGGGGCAGATCAGTGAGAGGACACTTG   2040
ATGGAAAGCAATACACTTTAAGACTGAGCACAGTTTCGTGCTCAGCTCTGTCTGGTGCTG   2100
TGAGCTAGAGAAGCTCACCACATACATATAAAAATCAGAGGCTCATGTCCCTGTGGTTAG   2160
ACCCTACTCGCGGCGGTGTACTCCACCACAGCAGCACCGCACCGCTGGAAGTACAGTGCT   2220
GTCTTCAACAGGTGTGAAAGAACCTGAGCTGAGGGTGACAGTGCCCAGGGGAACCCTGCT   2280
TGCAGTCTATTGCATTTACATACCGCATTTCAGGGCACATTAGCATCCACTCCTATGGTA   2340
GCACACTGTTGACAATAGGACAAGGGATAGGGGTTGACTATCCCTTATCCAAAATGCTTG   2400
GGACTAGAAGAGTTTTGGATTTTAGAGTCTTTTCAGGCATAGGTATATTTGAGTATATAT   2460
AAAATGAGATATCTTGGGGATGGGGCCCAAGTATAAACATGAAGTTCATTTATATTTCAT   2520
AATACCGTATAGACACTGCTTGAAGTGTAGTTTTATACAGTGTTTTAAATAACGTTGTAT   2580
GCATGAAAGACGTTTTTACAGCATGAACCTGTCTACTCATGCCAGCACTCAAAAACCTTG   2640
GGGTTTTGGAGCAGTTTGGATCTTGGGTTTTCTGTTAAGAGATGGTTAGCTTATACCTAA   2700
AACCATAATGGCAAACAGGCTGCAGGACCAGACTGGATCCTCAGCCCTGAAGTGTGCCCT   2760
TCCAGCCAGGTCATACCCTGTGGAGGTGAGCGGGATCAGGTTTTGTGGTGCTAAGAGAGG   2820
AGTTGGAGGTAGATTTTGGAGGATCTGAGGGC                               2852
```

```
---G--GTTG CAAGGCCCAA GAAGCCCA-- -TCCTGGGAA GGAAAATGCA      50
TTGGGGAACC CTGTG-CGGA TTCTTGTGGC TTTGGCCCTA TCTTTTCTAT     100
GTCCAAGCTG TGCCCATCCA AAAAGTCCAA GATGACACCA AAACCCTCAT     150
CAAGACAATT GTCACCAGGA TCAATGACAT TTCACACACG CAGTCAGTCT     200
CCTCCAAACA GAAAGTCACC GGTTTGGACT TCATTCCTGG GCTCCACCCC     250
ATCCTGACCT TATCCAAGAT GGACCAGACA CTGGCAGTCT ACCAACAGAT     300
CCTCACCAGT ATGCCTTCCA GAAACGTGAT CCAAATATCC AACGACCTGG     350
AGAACCTCCG GGATCTTCTT CACGTGCTGG CCTTCTCTAA GAGCTGCCAC     400
TTGCCCTGGG CCAGTGGCCT GGAGACCTTG GACAGCCTGG GGGGTGTCCT     450
GGAAGCTTCA GGCTACTCCA CAGAGGTGGT GGCCCTGAGC AGGCTGCAGG     500
GGTCTCTGCA GGACATGCTG TGGCAGCTGG ACCTCAGCCC TGGGTGCTGA     550
GGCCTTGAAG GTCACTCTTC CTGCAAGGAC T-ACGTTAAG GGAAGGAACT     600
CTGGTTTCCA GGTATCTCCA GGATTGAAGA GCATTGCATG GACACCCCTT     650
ATCCAGGACT CTGTCAATTT CCCTGACTCC TCTAAGCCAC TCTTCCAAAG     700
G                                                         701
```

FIG.2

```
  1  MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR
 16  LEU PHE TYR VAL GLN ALA VAL PRO ILE GLN LYS VAL GLN ASP ASP
 31  THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
 46  SER HIS THR GLN SER VAL SER SER LYS GLN LYS VAL THR GLY LEU
 61  ASP PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET
 76  ASP GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO
 91  SER ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG
106  ASP LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO
121  TRP ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU
136  GLU ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU
151  GLN GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO
166  GLY CYS END
```

FIG. 3

```
MOUSE   MCWRPLCRFL WLWSYLSYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS    50
        * **  *      *  *
HUMAN   MHWGTLCGFL WLWPYLFYVQ AVPIQKVQDD TKTLIKTIVT RINDISHTQS

MOUSE   VSAKQRVTGL DFIPGLHPIL SLSKMDQTLA VYQQVLTSLP SQNVLQIAND   100
          *                    -                 -  -  *     *
HUMAN   VSSKQKVTGL DFIPGLHPIL TLSKMDQTLA VYQQILTSMP SRNVIQISND

MOUSE   LENLRDLLHL LAFSKSCSLP QTSGLQKPES LDGVLEASLY STEVVALSRL   150
                -          *   **   ***-   *       *
HUMAN   LENLRDLLHV LAFSKSCHLP WASGLETLDS LGGVLEASGY STEVVALSRL

MOUSE   QGSLQDILQQ LDVSPEC                                       167
              - *   -  *
HUMAN   QGSLQDMLWQ LDLSPGC
```

FIG.4

1	MET CYS TRP ARG PRO LEU CYS ARG PHE LEU TRP LEU TRP SER TYR
16	LEU SER TYR VAL GLN ALA VAL PRO ILE GLN LYS VAL GLN ASP ASP
31	THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46	SER HIS THR SER VAL SER ALA LYS GLN ARG VAL THR GLY LEU ASP
61	PHE ILE PRO GLY LEU HIS PRO ILE LEU SER LEU SER LYS MET ASP
76	GLN THR LEU ALA VAL TYR GLN GLN VAL LEU THR SER LEU PRO SER
91	GLN ASN VAL LEU GLN ILE ALA ASN ASP LEU GLU ASN LEU ARG ASP
106	LEU LEU HIS LEU LEU ALA PHE SER LYS SER CYS SER LEU PRO GLN
121	THR SER GLY LEU GLN LYS PRO GLU SER LEU ASP GLY VAL LEU GLU
136	ALA SER LEU TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU GLN
151	GLY SER LEU GLN ASP ILE LEU GLN GLN LEU ASP VAL SER PRO GLU
166	CYS END

FIG.5

1	MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR
16	LEU PHE TYR VAL GLN ALA VAL PRO ILE GLN LYS VAL GLN ASP ASP
31	THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46	SER HIS THR SER VAL SER SER LYS GLN LYS VAL THR GLY LEU ASP
61	PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET ASP
76	GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO SER
91	ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG ASP
106	LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO TRP
121	ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU GLU
136	ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU GLN
151	GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO GLY
166	CYS END

FIG.6

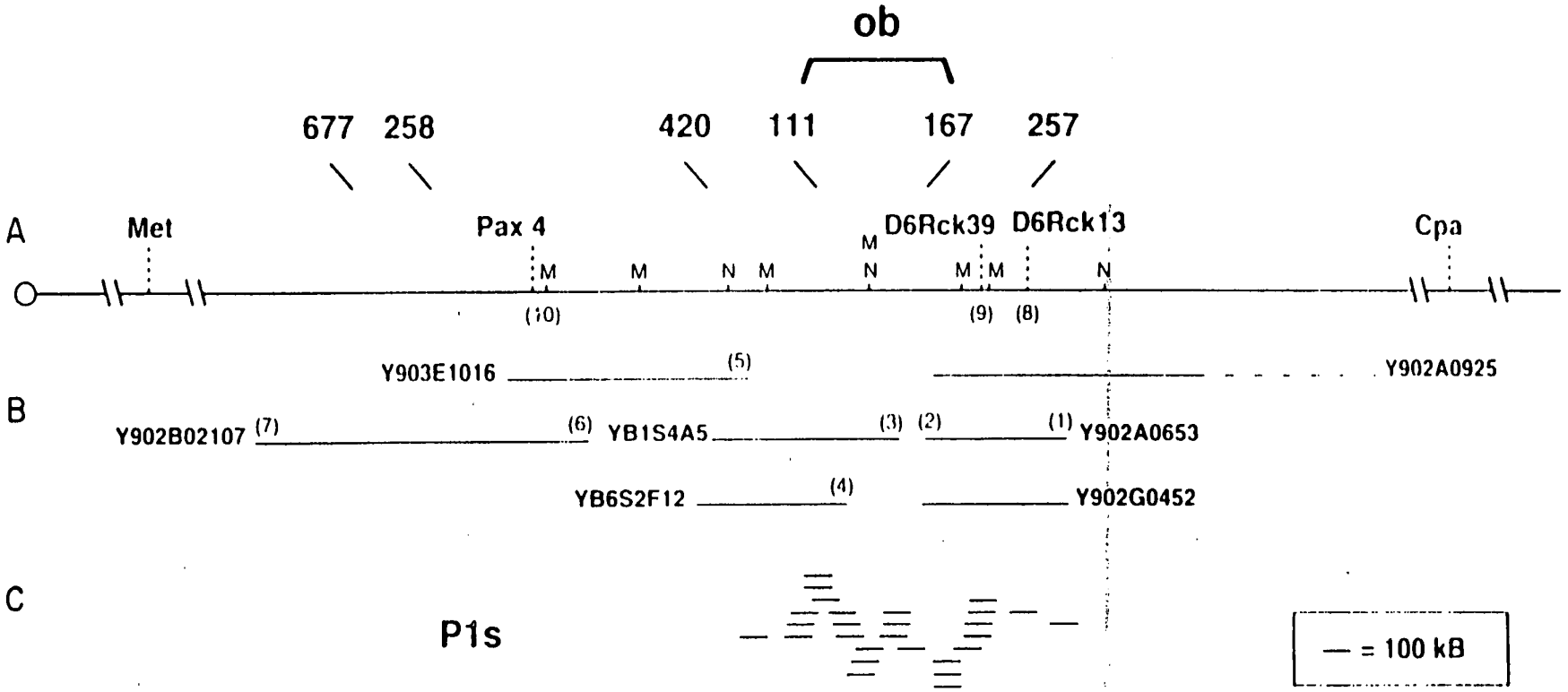

ob
677
258
420
111
167
257
A
Met
Pax 4
D6Rck39
D6Rck13
Cpa
M
M
N
M
N
M
M
N
(10)
(9)
(8)
Y903E1016
(5)
Y902A0925
B
Y902B02107
(7)
(6)
YB1S4A5
(3)
(2)
(1)
Y902A0653
YB6S2F12
(4)
Y902G0452
C
P1s
— = 100 kB

FIG.7

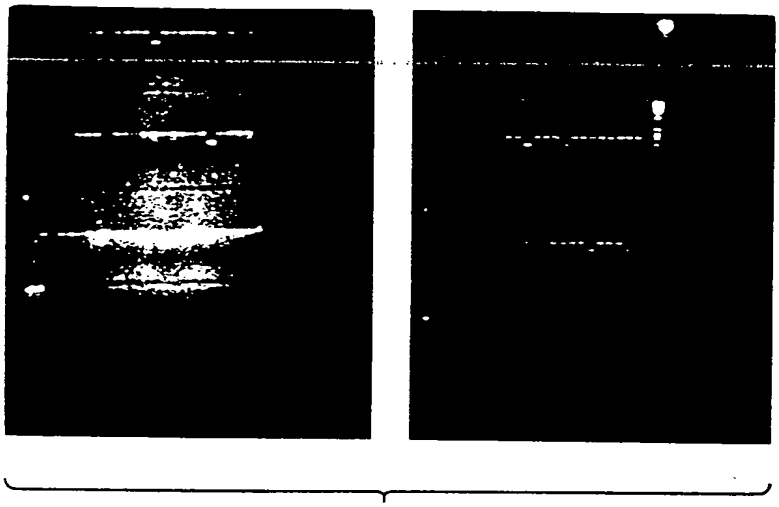


FIG.8

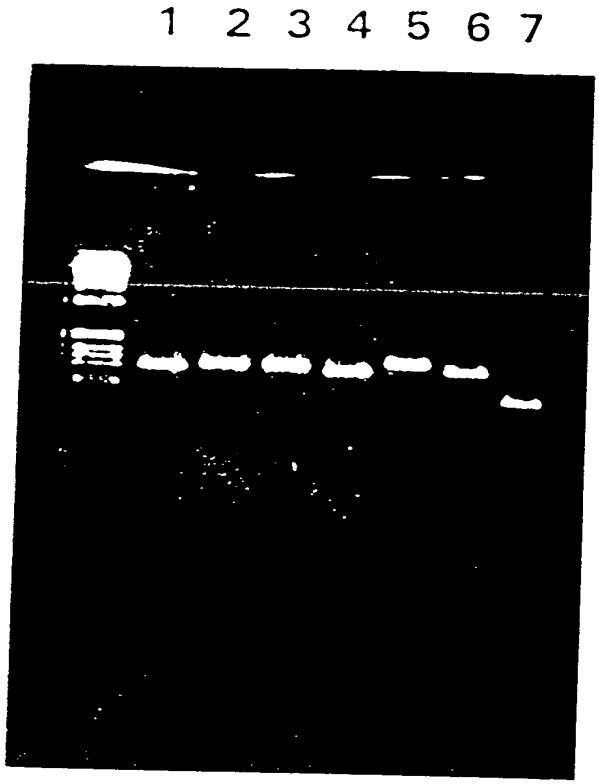


FIG.9

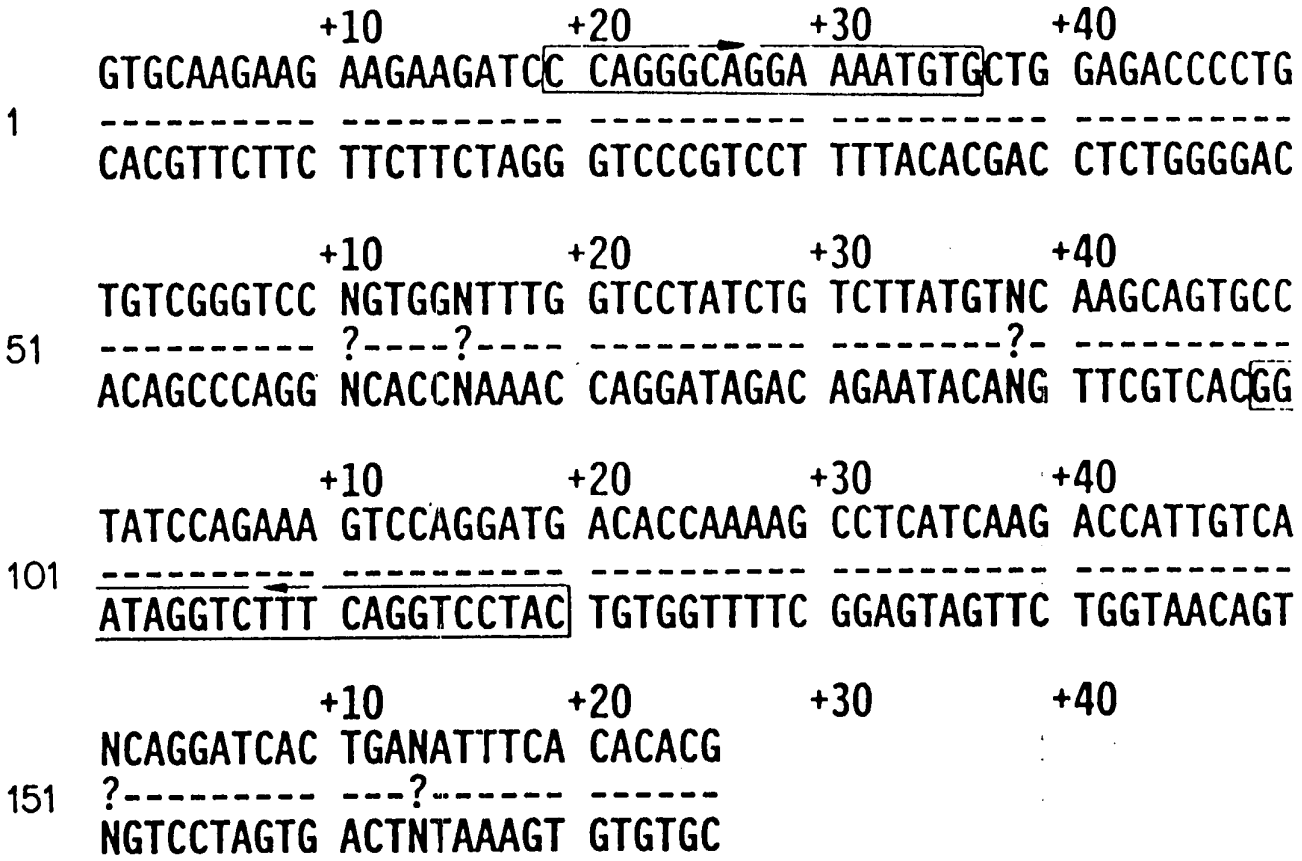

+10 +20 +30 +40
GTGCAAGAAG AAGAAGATCC CAGGGCAGGA AAATGTGCTG GAGACCCCTG
1
CACGTTCTTC TTCTTCTAGG GTCCCGTCCT TTTACACGAC CTCTGGGGAC
+10 +20 +30 +40
TGTCGGGTCC NGTGGNTTTG GTCCTATCTG TCTTATGTNC AAGCAGTGCC
51
ACAGCCCAGG NCACCNAAAC CAGGATAGAC AGAATACANG TTCGTCACGG
+10 +20 +30 +40
TATCCAGAAA GTCCAGGATG ACACCAAAAG CCTCATCAAG ACCATTGTCA
101
ATAGGTCTTT CAGGTCCTAC TGTGGTTTTC GGAGTAGTTC TGGTAACAGT
+10 +20 +30 +40
NCAGGATCAC TGANATTTCA CACACG
151
NGTCCTAGTG ACTNTAAAGT GTGTGC

FIG.10

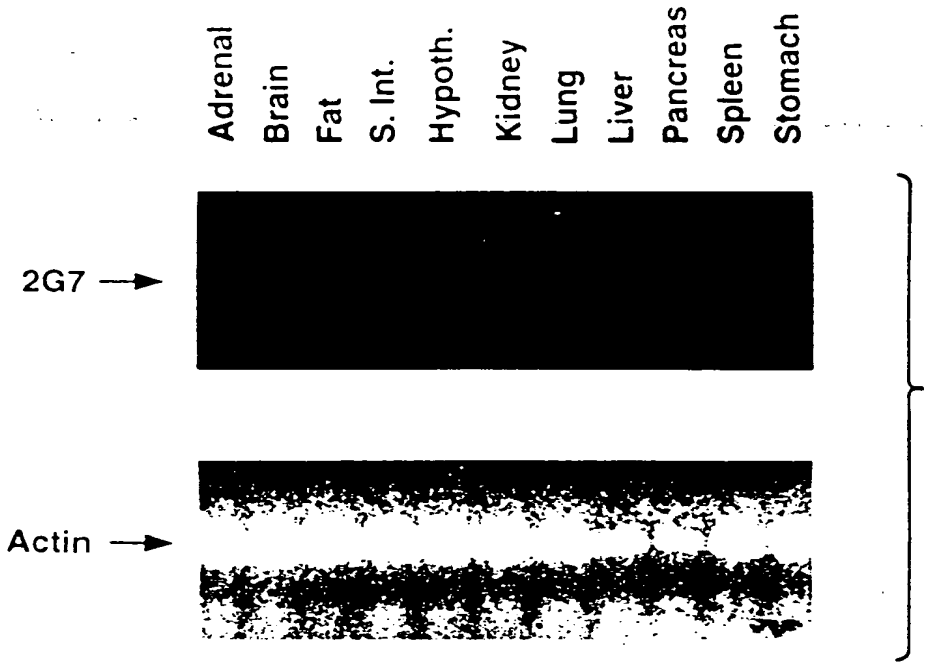

Adrenal
Brain
Fat
S. Int.
Hypoth.
Kidney
Lung
Liver
Pancreas
Spleen
Stomach
2G7
Actin

FIG.11A

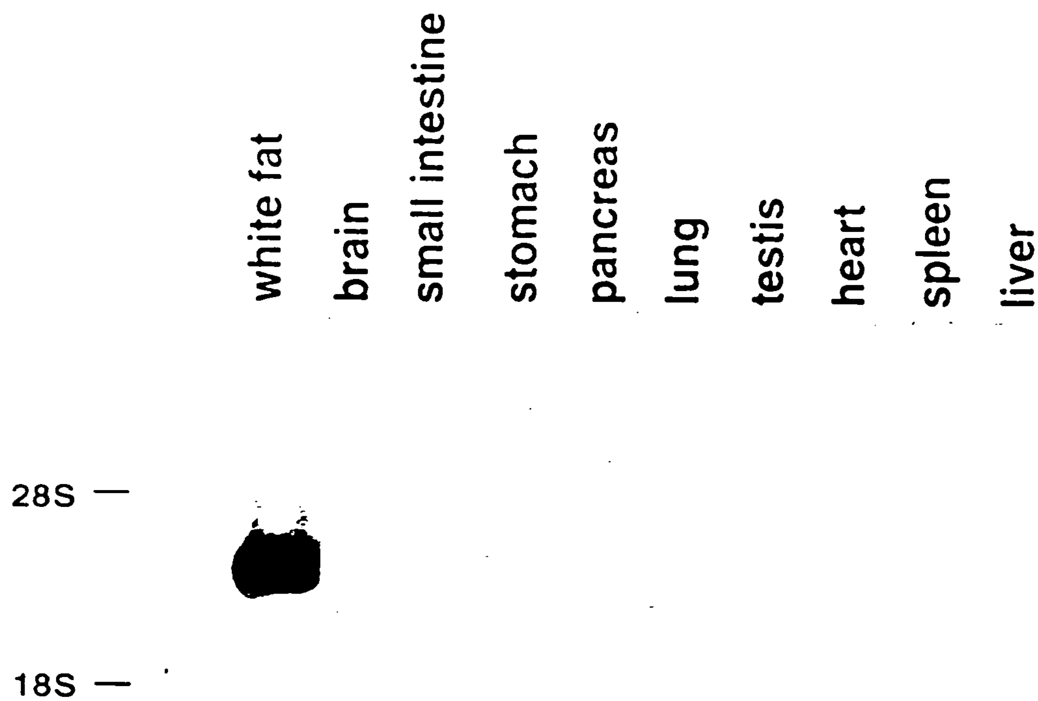

white fat
brain
small intestine
stomach
pancreas
lung
testis
heart
spleen
liver
28S
18S

FIG.11B

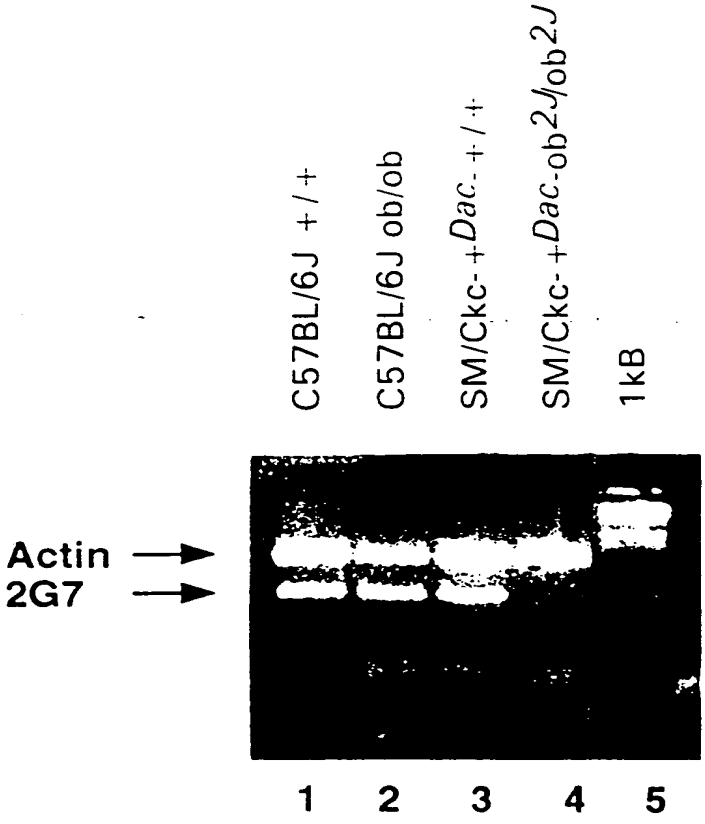

C57BL/6J +/+
C57BL/6J ob/ob
SM/Ckc-+Dac-+/+
SM/Ckc-+Dac-obJ/obJ
1kB
Actin
2G7
1
2
3
4
5

FIG.12A

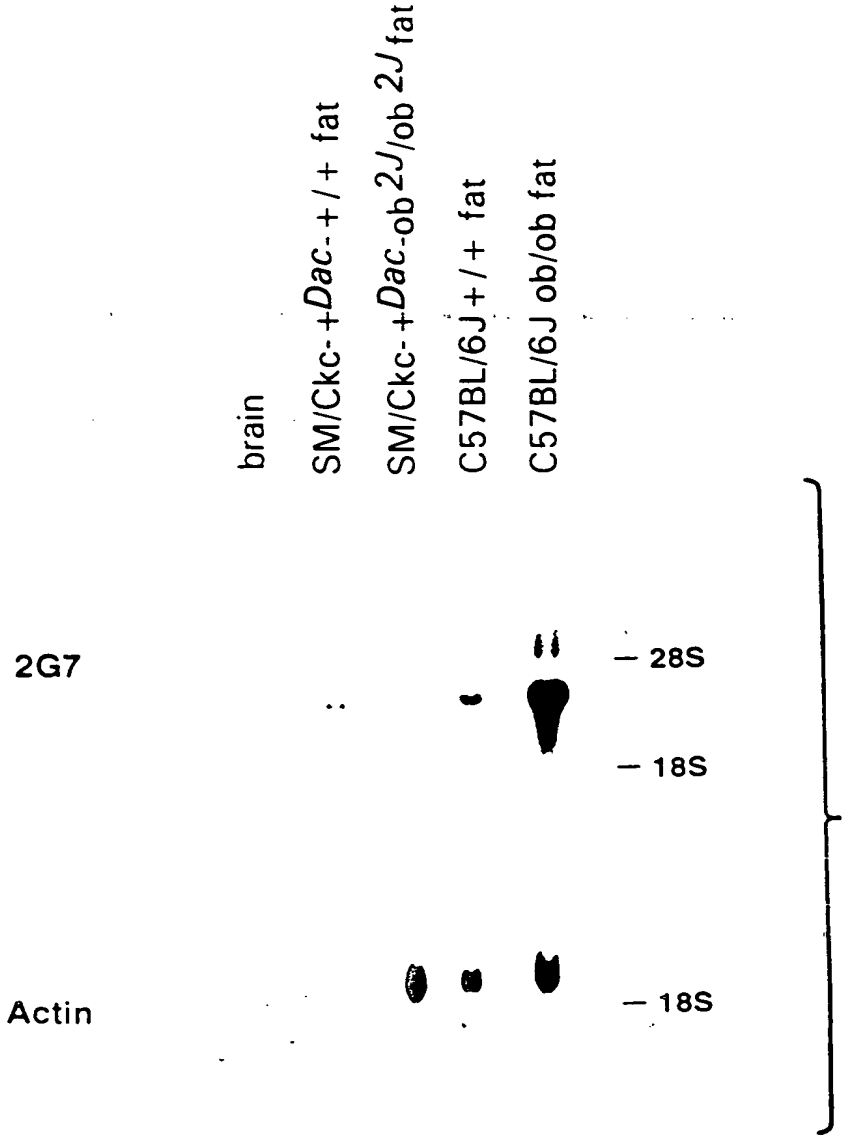

brain
SM/Ckc-+Dac-+/+ fat
SM/Ckc-+Dac-ob 2J/ob 2J fat
C57BL/6J+/+ fat
C57BL/6J ob/ob fat
2G7
28S
18S
Actin
18S

FIG. 12B

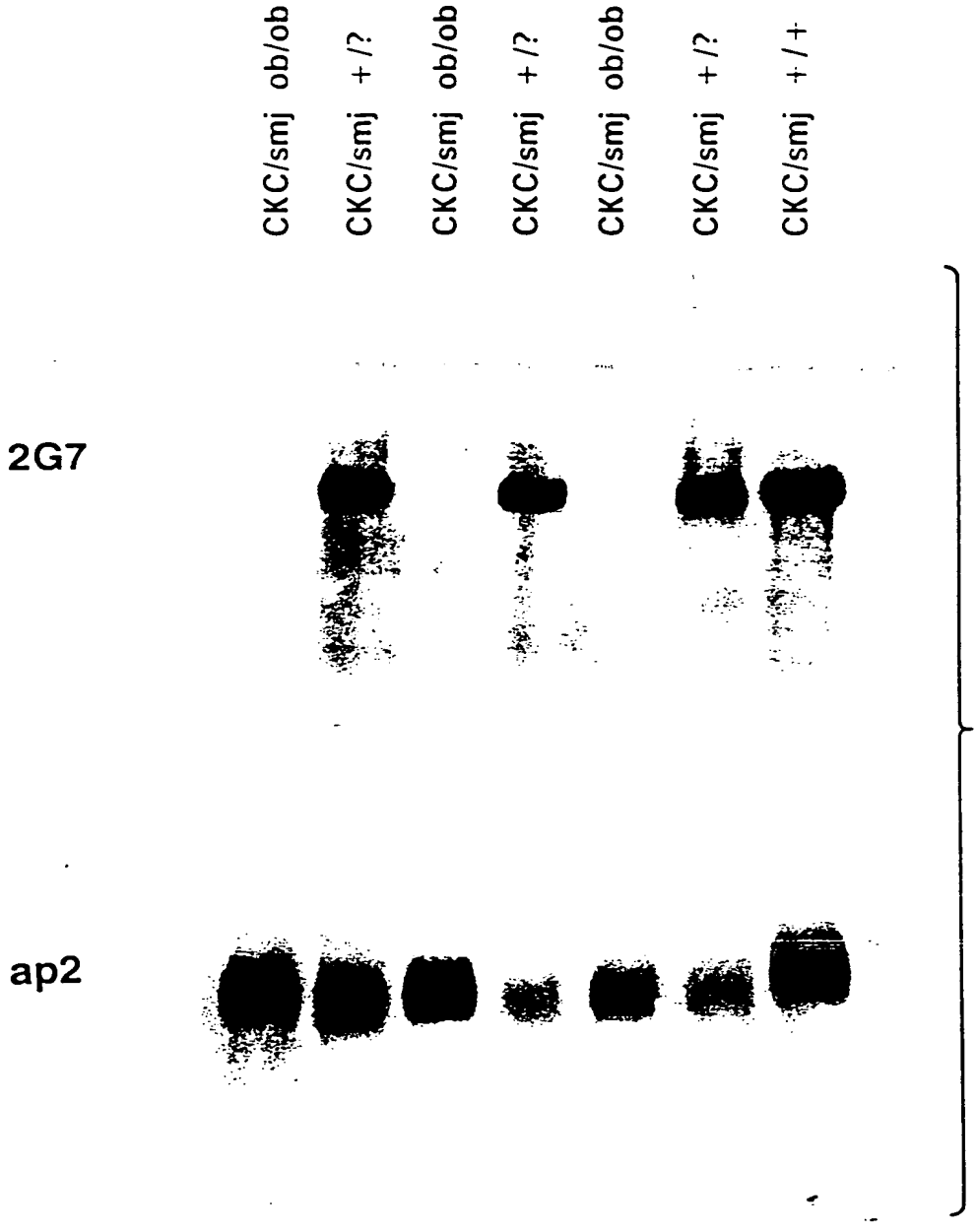

CKC/smj ob/ob
CKC/smj +/?
CKC/smj ob/ob
CKC/smj +/?
CKC/smj ob/ob
CKC/smj +/?
CKC/smj +/+
2G7
ap2

FIG. 13

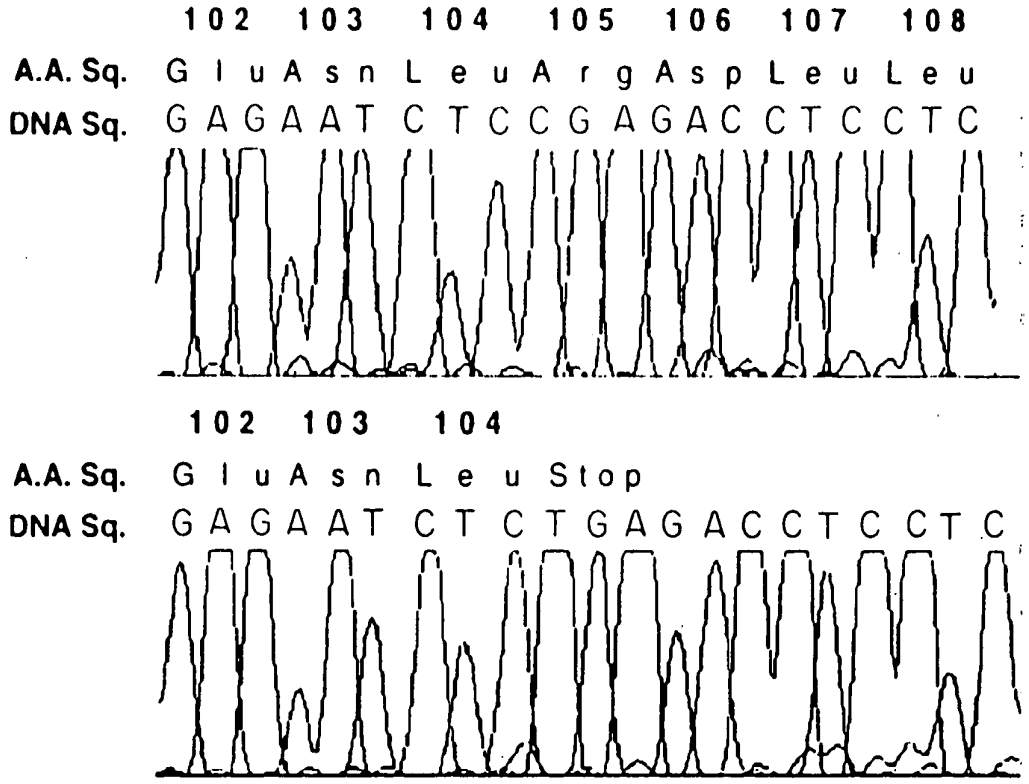

102 103 104 105 106 107 108
A.A. Sq. GluAsnLeuArgAspLeuLeu
DNA Sq. GAGAATCTCCGAGACCTCCTC
C57BL/6J
102 103 104
A.A. Sq. GluAsnLeuStop
DNA Sq. GAGAATCTCTGAGACCTCCTC
C57BL/6J ob/ob

FIG.14

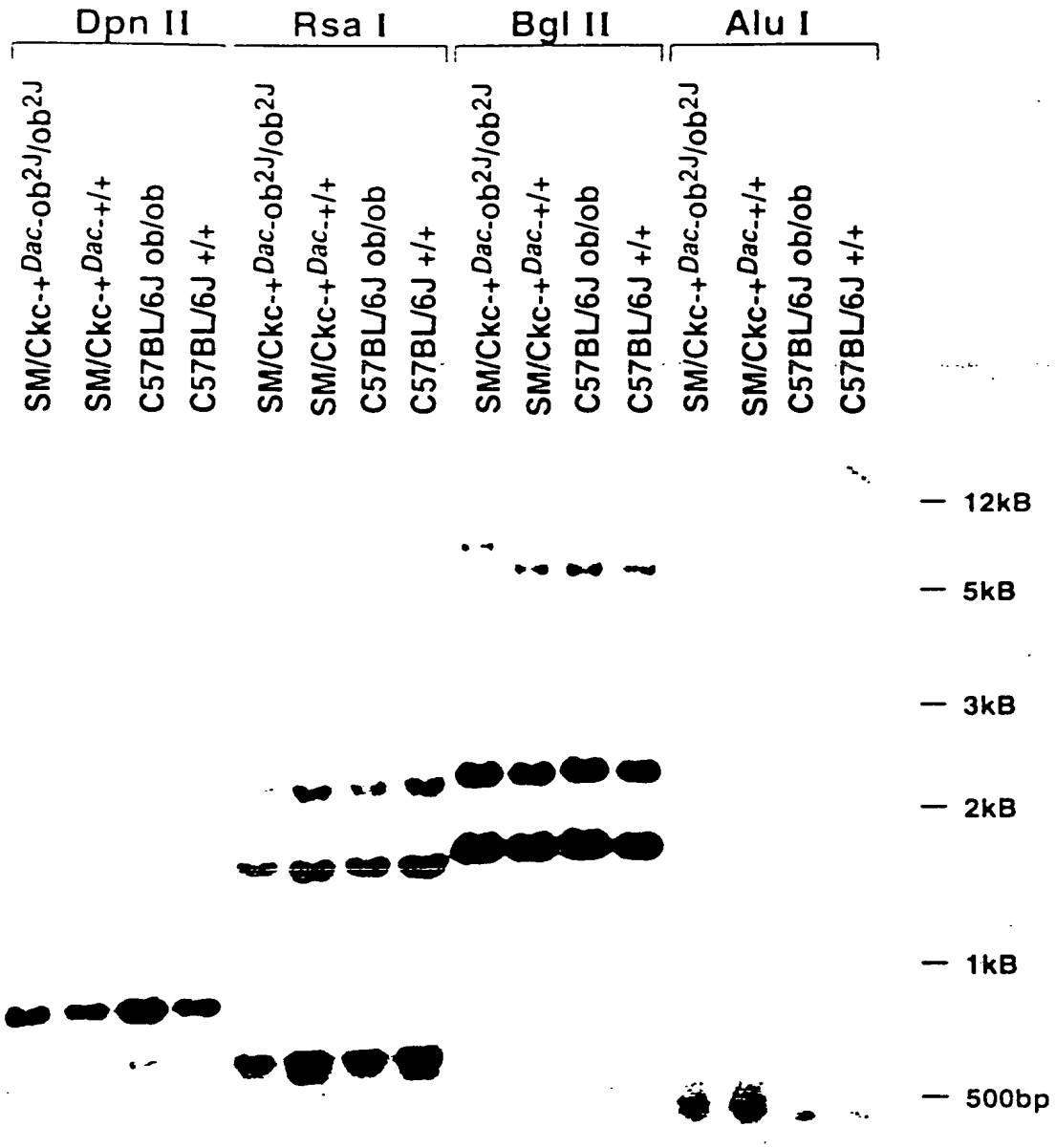

Dpn II
Rsa I
Bgl II
Alu I
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
C57BL/6J +/+
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
C57BL/6J +/+
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
C57BL/6J +/+
SM/Ckc-+Dac-ob2J/ob2J
SM/Ckc-+Dac-+/+
C57BL/6J ob/ob
C57BL/6J +/+
12kB
5kB
3kB
2kB
1kB
500bp

FIG.15A

BglII Digests

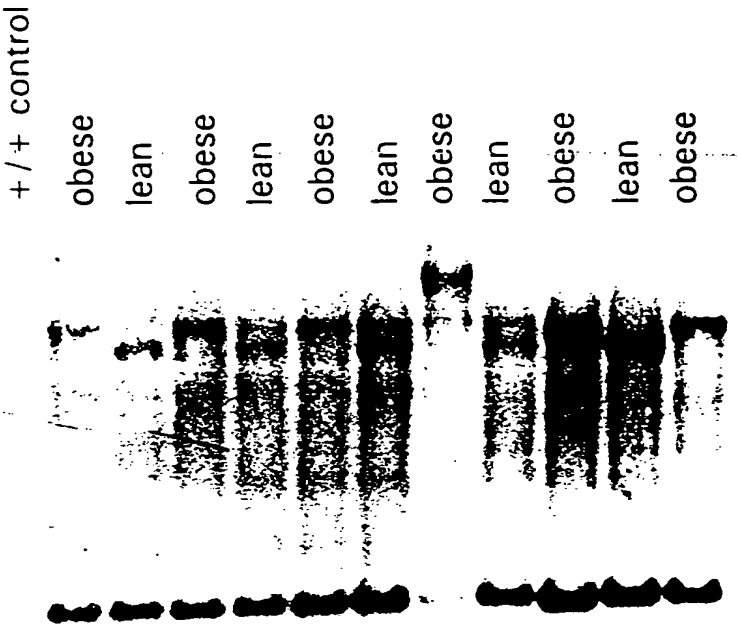


FIG.15B

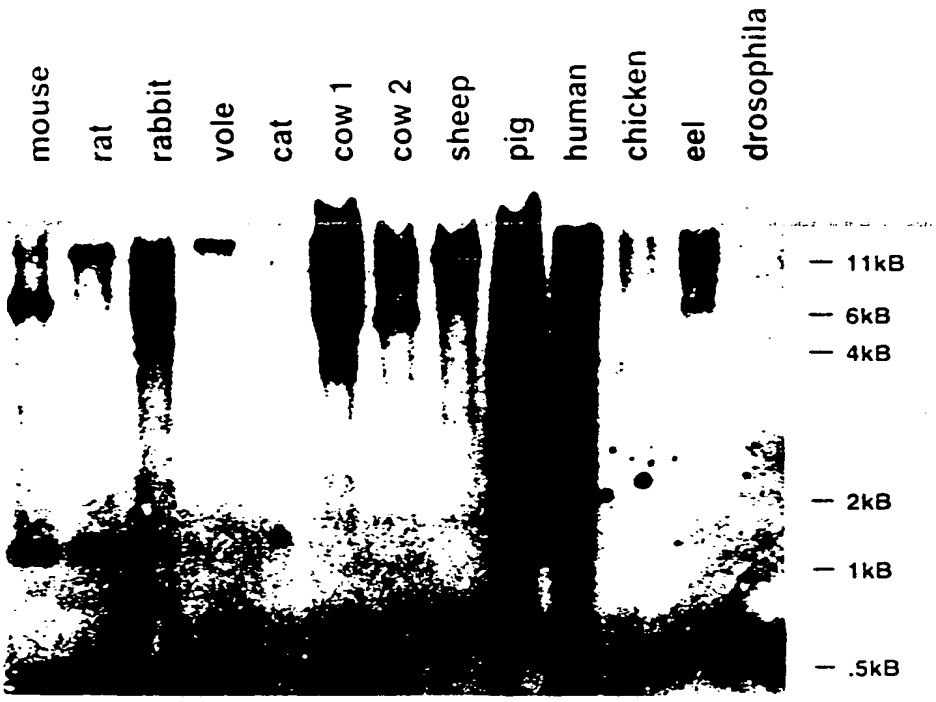

mouse
rat
rabbit
vole
cat
cow 1
cow 2
sheep
pig
human
chicken
eel
drosophila
11kB
6kB
4kB
2kB
1kB
.5kB

FIG.16

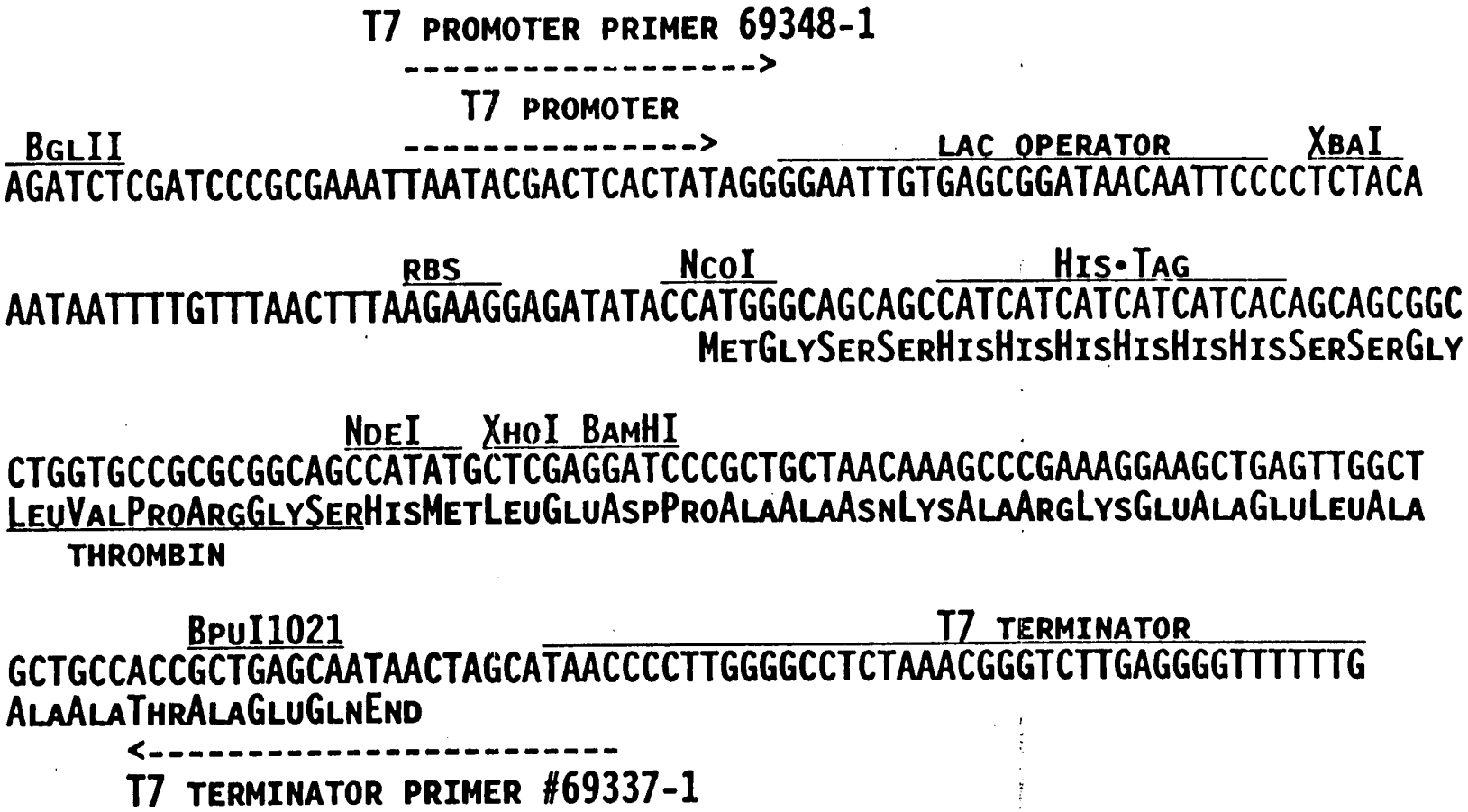

T7 PROMOTER PRIMER 69348-1
T7 PROMOTER
BGLII
LAC OPERATOR
XBAI
AGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTACA
RBS
NCOI
HIS•TAG
AATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGC
METGLYSERSERHISHISHISHISHISHISSERSERGLY
NDEI
XHOI
BAMHI
CTGGTGCCGCGCGGCAGCCATATGCTCGAGGATCCCGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCT
LEUVALPROARGGLYSERHISMETLEUGLUASPPROALAALAASNLYSALAARGLYSGLUALAGLULEUALA
THROMBIN
BPUI1021
T7 TERMINATOR
GCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
ALAALATHRALAGLUGLNEND
T7 TERMINATOR PRIMER #69337-1

FIG.17

FIG. 18A

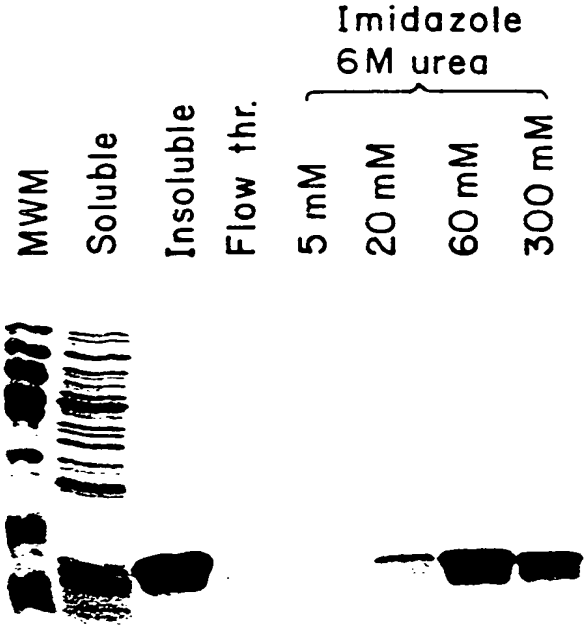


FIG. 18B

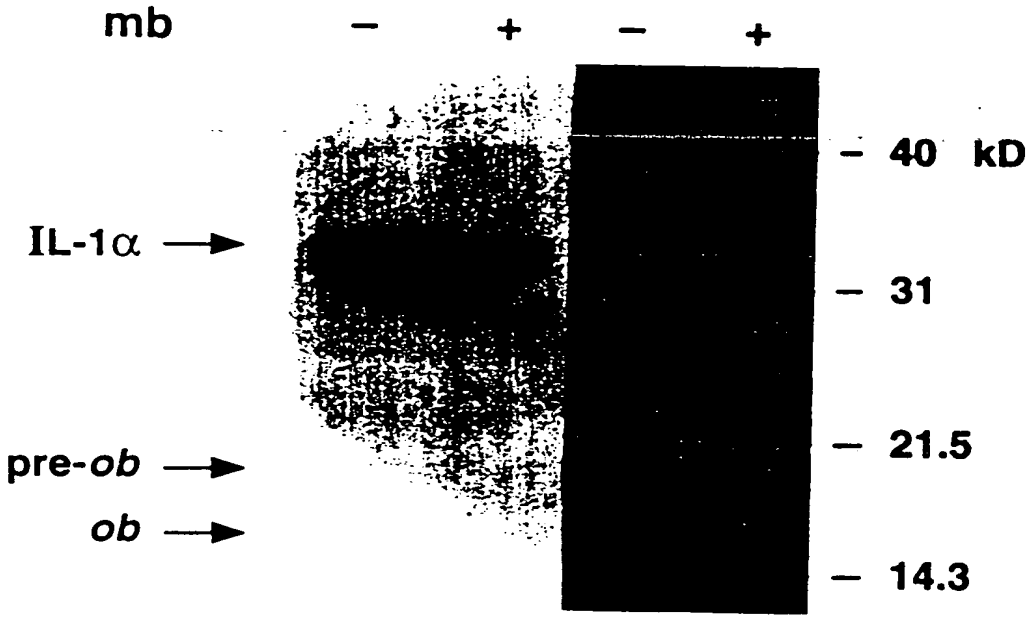


FIG.19A

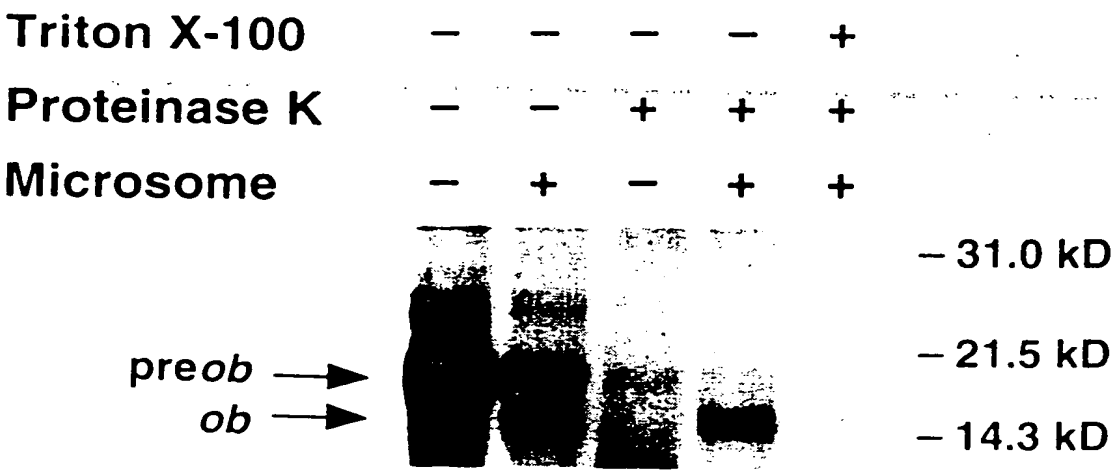

Triton X-100 – – – – +
Proteinase K – – + + +
Microsome – + – + +
preob
ob
– 31.0 kD
– 21.5 kD
– 14.3 kD

FIG.19B

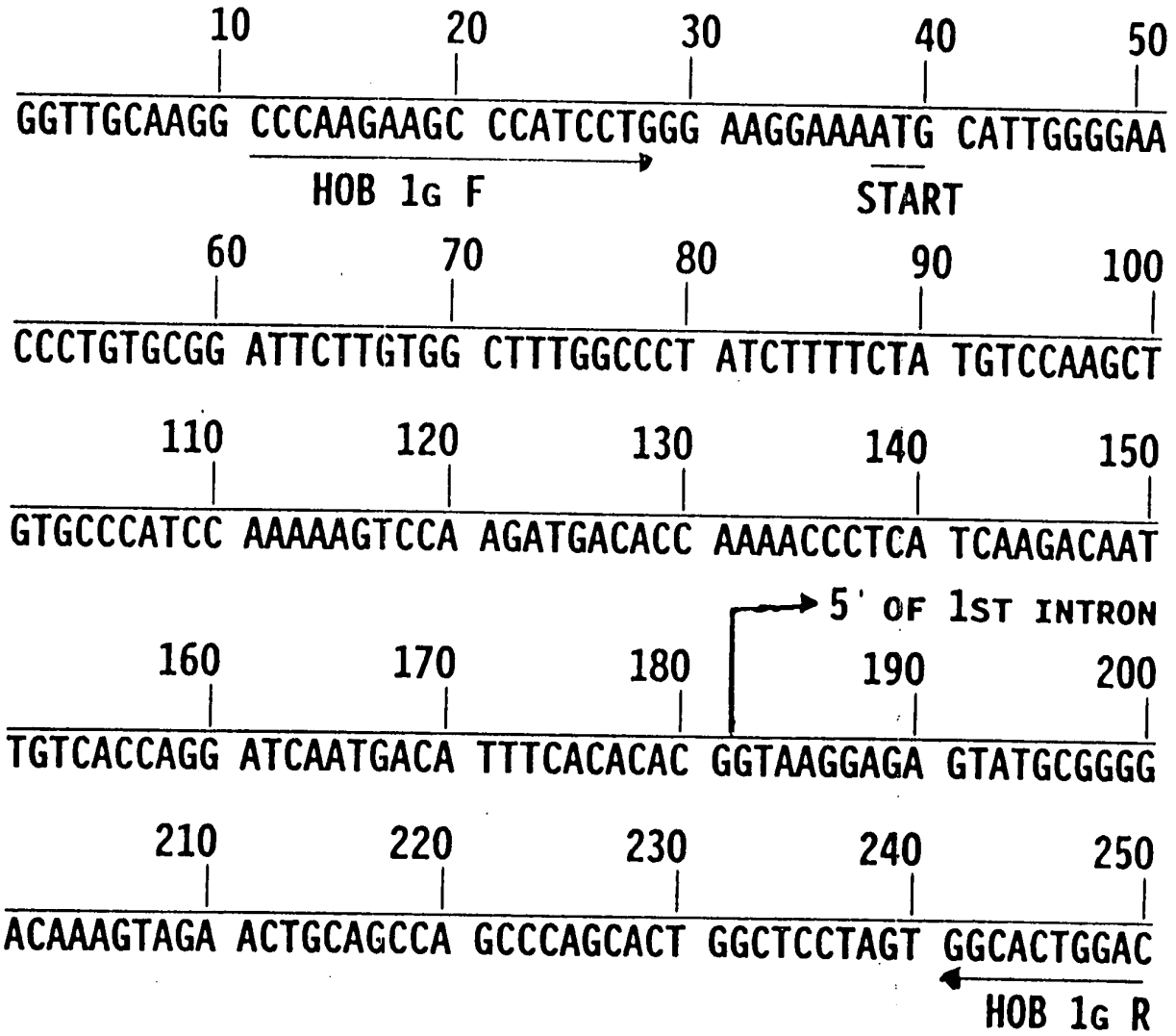

10
20
30
40
50
GGTTGCAAGG CCCAAGAAGC CCATCCTGGG AAGGAAAATG CATTGGGGAA
HOB 1G F
START
60
70
80
90
100
CCCTGTGCGG ATTCTTGTGG CTTTGGCCCT ATCTTTTCTA TGTCCAAGCT
110
120
130
140
150
GTGCCCATCC AAAAAGTCCA AGATGACACC AAAACCCTCA TCAAGACAAT
5' OF 1ST INTRON
160
170
180
190
200
TGTCACCAGG ATCAATGACA TTTCACACAC GGTAAGGAGA GTATGCGGGG
210
220
230
240
250
ACAAAGTAGA ACTGCAGCCA GCCCAGCACT GGCTCCTAGT GGCACTGGAC
HOB 1G R

FIG.20A-1

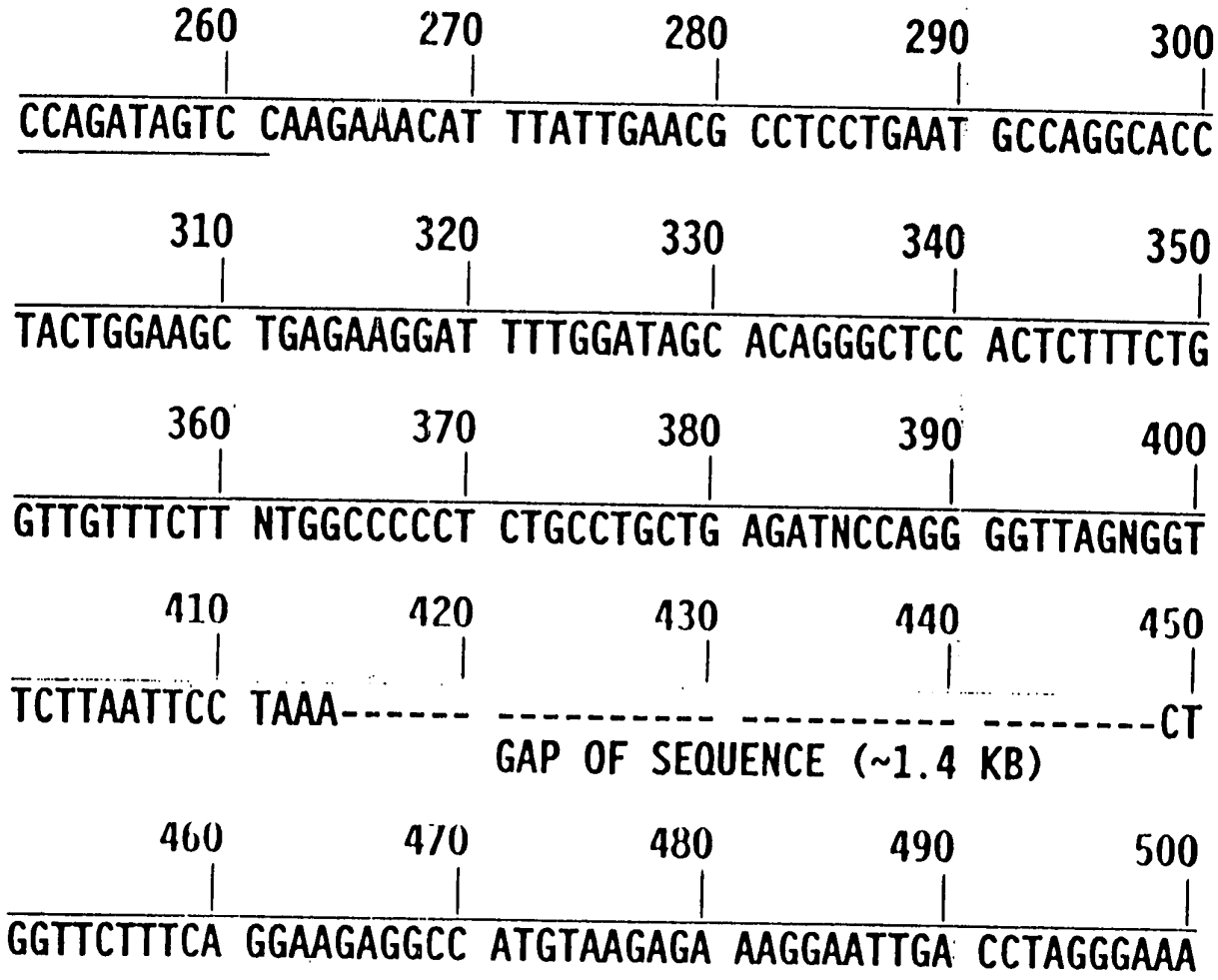

260
270
280
290
300
CCAGATAGTC CAAGAAACAT TTATTGAACG CCTCCTGAAT GCCAGGCACC
310
320
330
340
350
TACTGGAAGC TGAGAAGGAT TTTGGATAGC ACAGGGCTCC ACTCTTTCTG
360
370
380
390
400
GTTGTTTCTT NTGGCCCCCT CTGCCTGCTG AGATNCCAGG GGTTAGNGGT
410
420
430
440
450
TCTTAATTCC TAAA------ ---------- ---------- --------CT
GAP OF SEQUENCE (~1.4 KB)
460
470
480
490
500
GGTTCTTTCA GGAAGAGGCC ATGTAAGAGA AAGGAATTGA CCTAGGGAAA

FIG.20A - 2

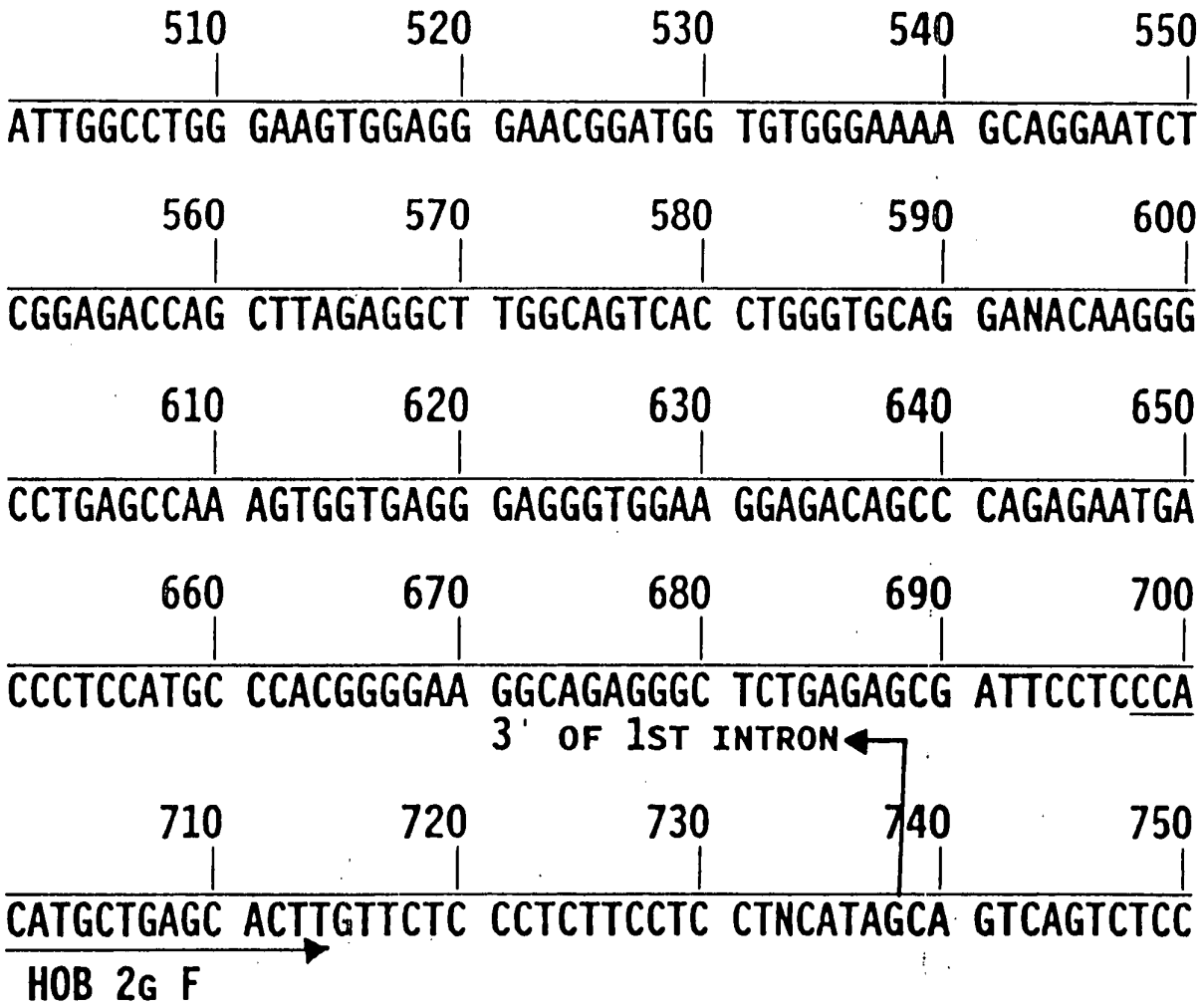

510 520 530 540 550
ATTGGCCTGG GAAGTGGAGG GAACGGATGG TGTGGGAAAA GCAGGAATCT
560 570 580 590 600
CGGAGACCAG CTTAGAGGCT TGGCAGTCAC CTGGGTGCAG GANACAAGGG
610 620 630 640 650
CCTGAGCCAA AGTGGTGAGG GAGGGTGGAA GGAGACAGCC CAGAGAATGA
660 670 680 690 700
CCCTCCATGC CCACGGGGAA GGCAGAGGGC TCTGAGAGCG ATTCCTCCCA
3' OF 1ST INTRON
710 720 730 740 750
CATGCTGAGC ACTTGTTCTC CCTCTTCCTC CTNCATAGCA GTCAGTCTCC
HOB 2G F

FIG.20A -3

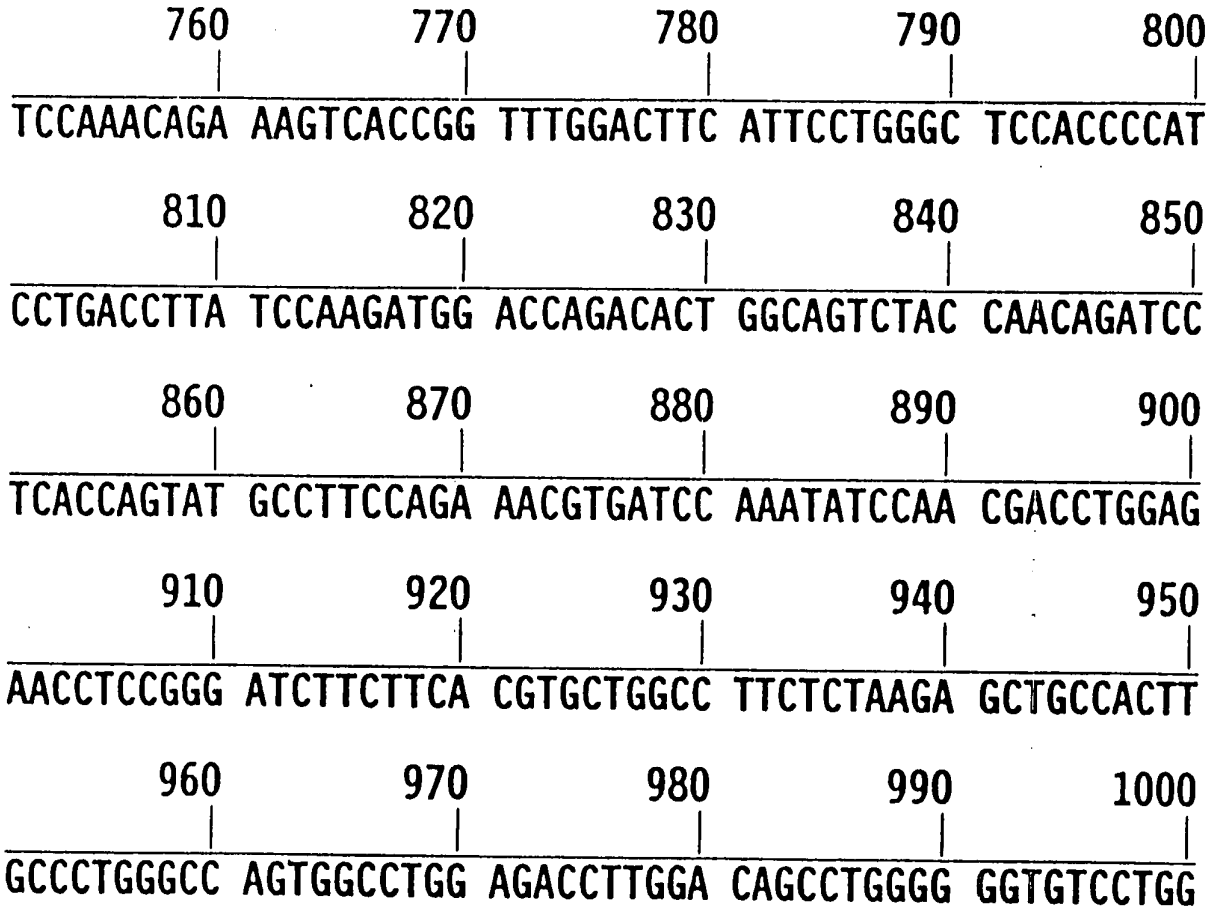

760 770 780 790 800
TCCAAACAGA AAGTCACCGG TTTGGACTTC ATTCCTGGGC TCCACCCCAT
810 820 830 840 850
CCTGACCTTA TCCAAGATGG ACCAGACACT GGCAGTCTAC CAACAGATCC
860 870 880 890 900
TCACCAGTAT GCCTTCCAGA AACGTGATCC AAATATCCAA CGACCTGGAG
910 920 930 940 950
AACCTCCGGG ATCTTCTTCA CGTGCTGGCC TTCTCTAAGA GCTGCCACTT
960 970 980 990 1000
GCCCTGGGCC AGTGGCCTGG AGACCTTGGA CAGCCTGGGG GGTGTCCTGG

FIG.20A -4

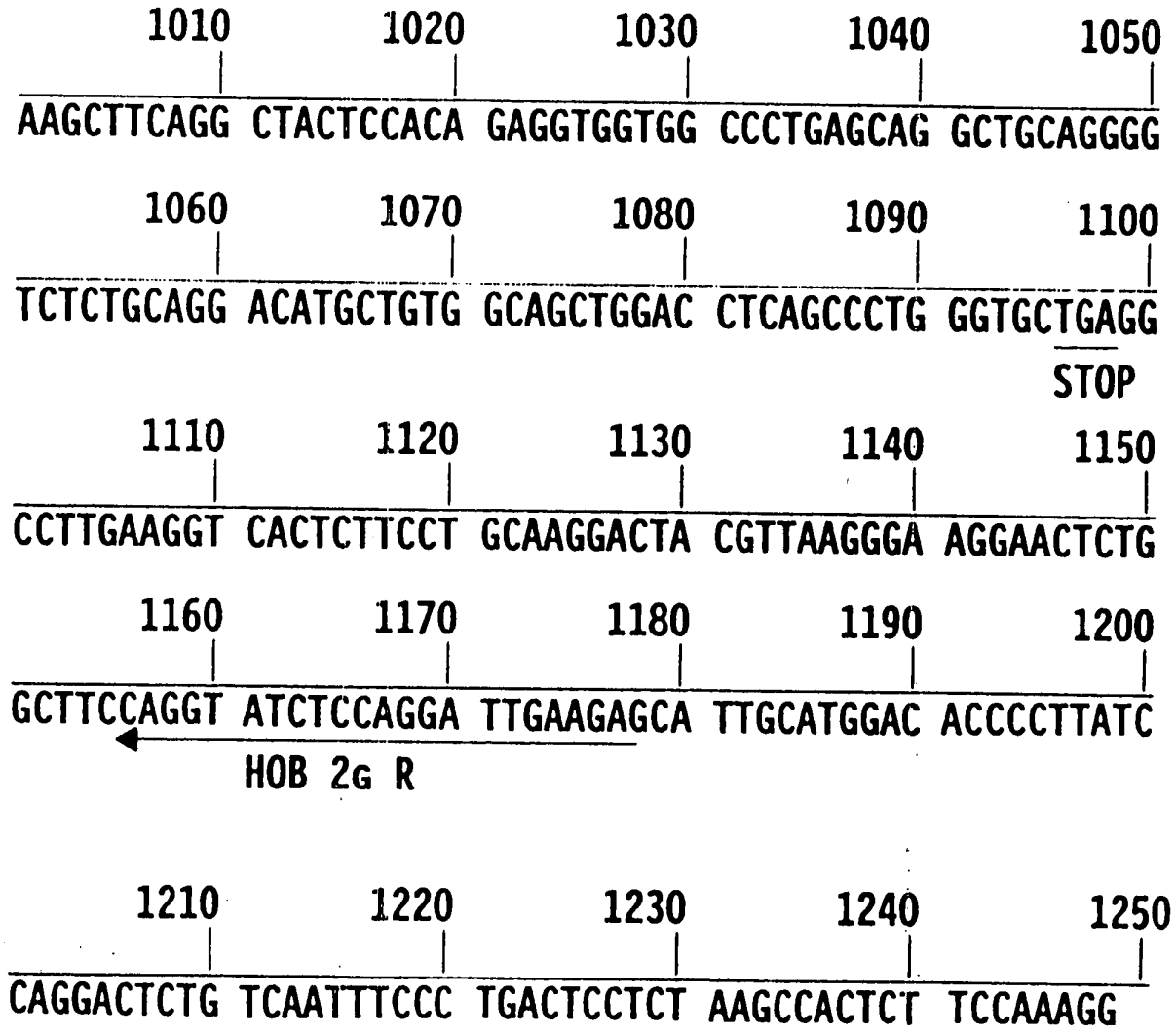

1010
1020
1030
1040
1050
AAGCTTCAGG CTACTCCACA GAGGTGGTGG CCCTGAGCAG GCTGCAGGGG
1060
1070
1080
1090
1100
TCTCTGCAGG ACATGCTGTG GCAGCTGGAC CTCAGCCCTG GGTGCTGAGG
STOP
1110
1120
1130
1140
1150
CCTTGAAGGT CACTCTTCCT GCAAGGACTA CGTTAAGGGA AGGAACTCTG
1160
1170
1180
1190
1200
GCTTCCAGGT ATCTCCAGGA TTGAAGAGCA TTGCATGGAC ACCCCTTATC
HOB 2G R
1210
1220
1230
1240
1250
CAGGACTCTG TCAATTTCCC TGACTCCTCT AAGCCACTCT TCCAAAGG

FIG.20A -5

MOUSE OB STRUCTURE

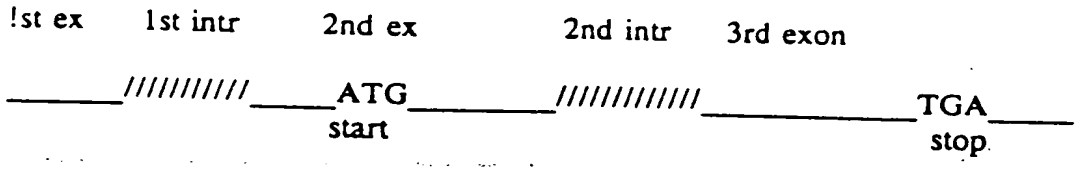


FIG.20B

HUMAN OB STRUCTURE

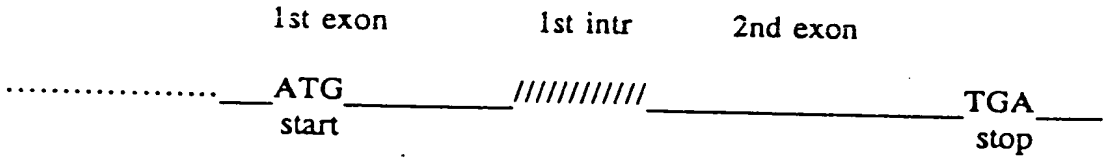


FIG.20C

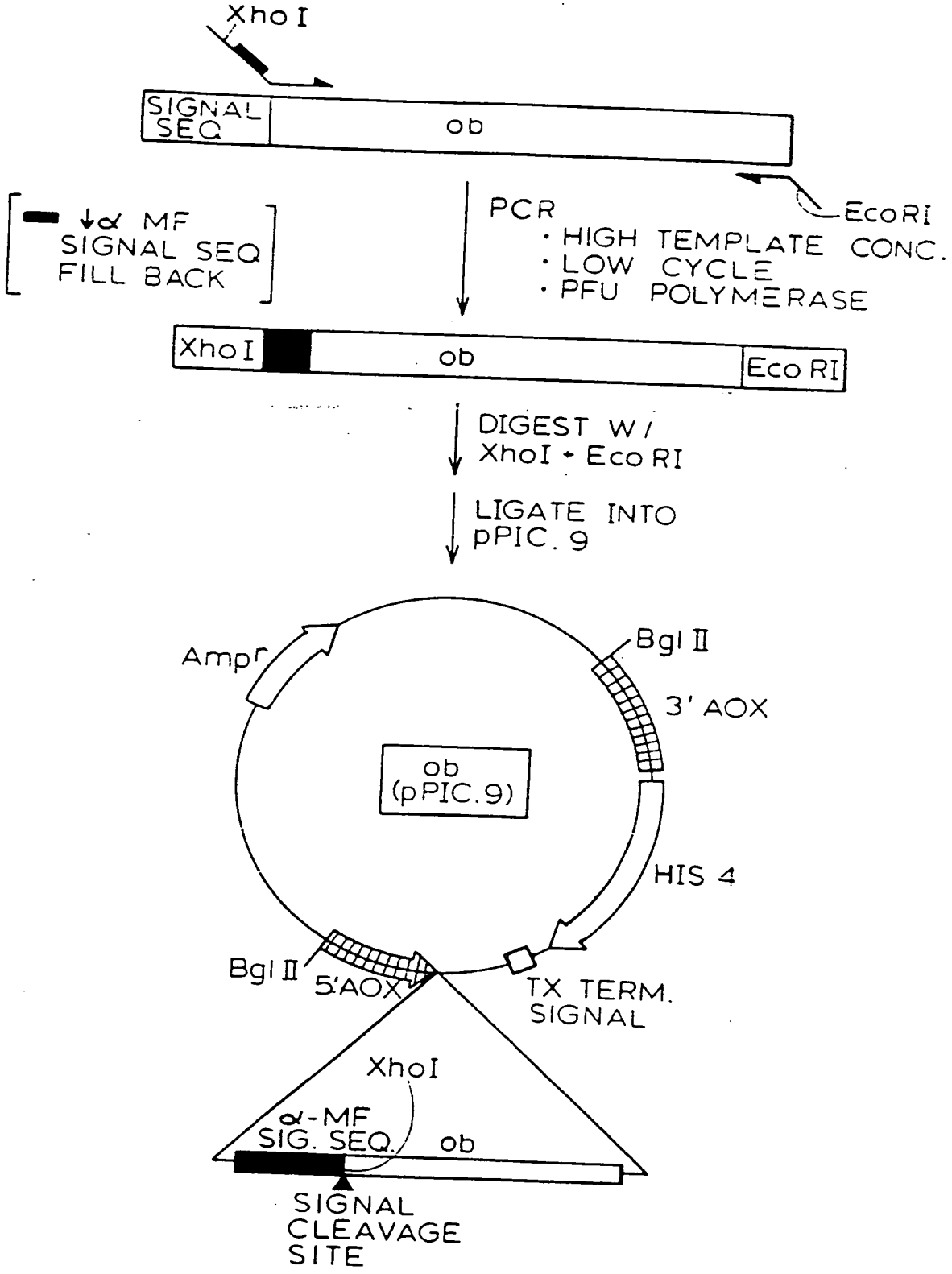

Xho I
SIGNAL SEQ
ob
EcoRI
[↓α MF SIGNAL SEQ FILL BACK]
PCR
· HIGH TEMPLATE CONC.
· LOW CYCLE
· PFU POLYMERASE
Xho I
ob
Eco RI
DIGEST W/ Xho I + Eco RI
LIGATE INTO pPIC. 9
Ampr
Bgl II
3' AOX
ob (pPIC.9)
HIS 4
Bgl II
5'AOX
TX TERM. SIGNAL
Xho I
α-MF SIG. SEQ.
ob
SIGNAL CLEAVAGE SITE

FIG.21A

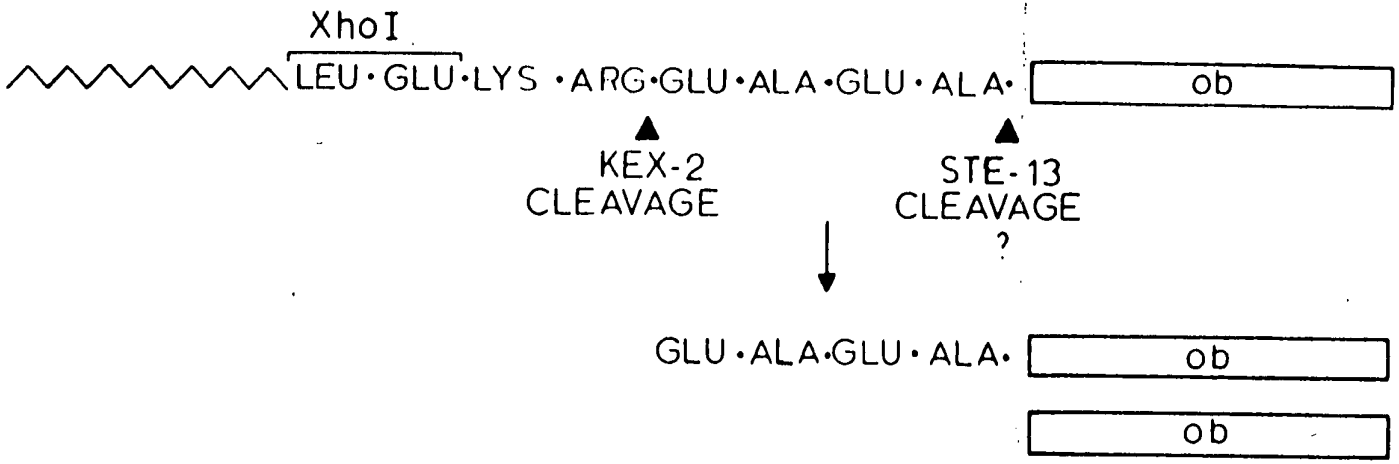


FIG.21B

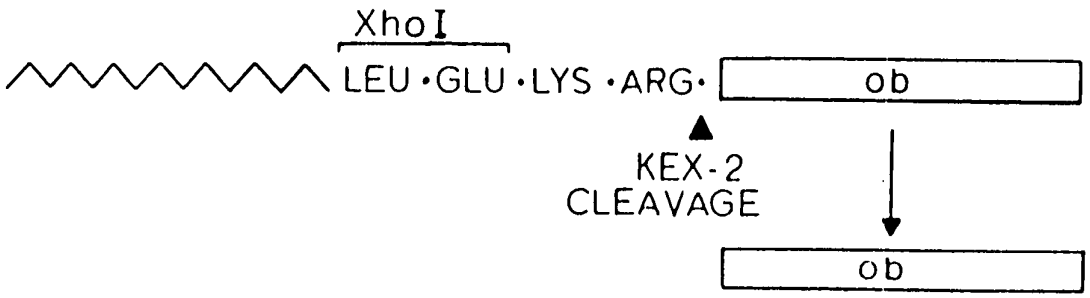


FIG.21C

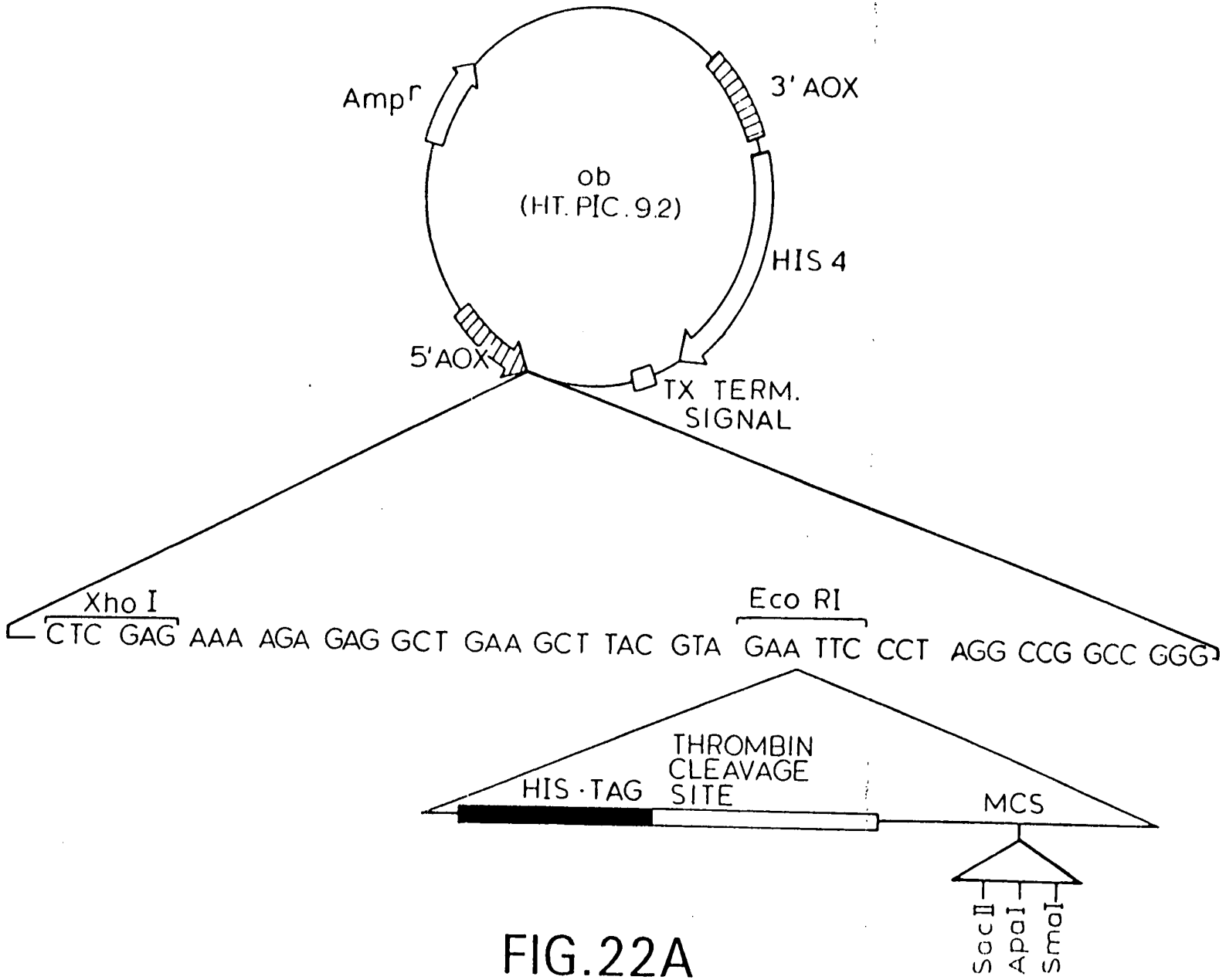

Amp^r
3' AOX
ob
(HT. PIC. 9.2)
HIS 4
5' AOX
TX TERM.
SIGNAL
Xho I
CTC GAG AAA AGA GAG GCT GAA GCT TAC GTA GAA TTC CCT AGG CCG GCC GGG
Eco RI
THROMBIN
CLEAVAGE
HIS · TAG
SITE
MCS
SacII
ApaI
SmaI

FIG.22A

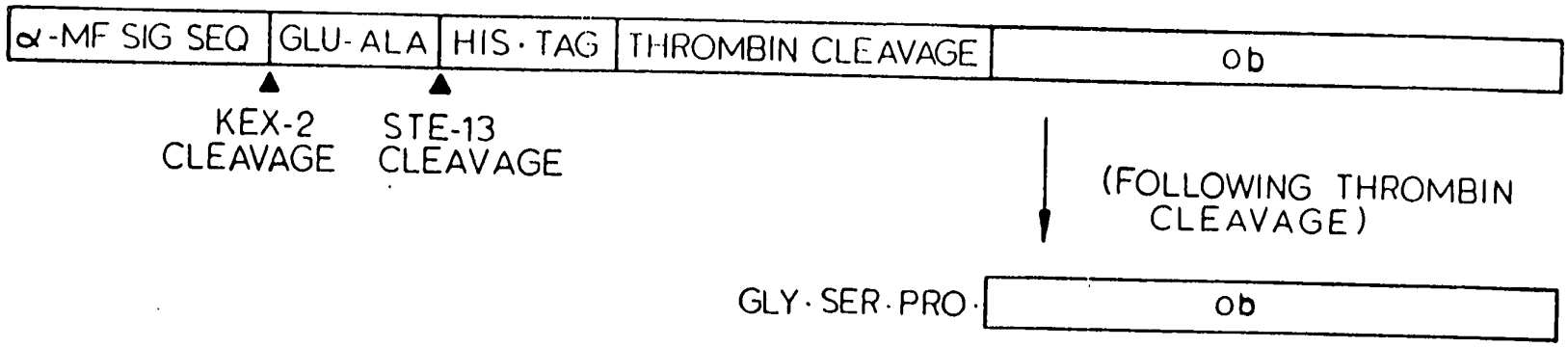

α-MF SIG SEQ
GLU-ALA
HIS·TAG
THROMBIN CLEAVAGE
ob
KEX-2 CLEAVAGE
STE-13 CLEAVAGE
(FOLLOWING THROMBIN CLEAVAGE)
GLY·SER·PRO·
ob

FIG.22B

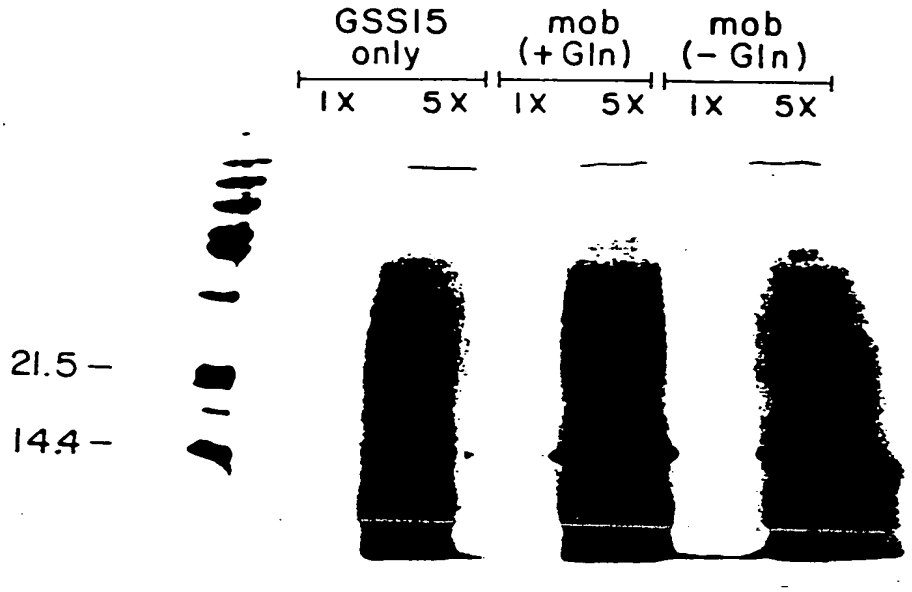


FIG.23A

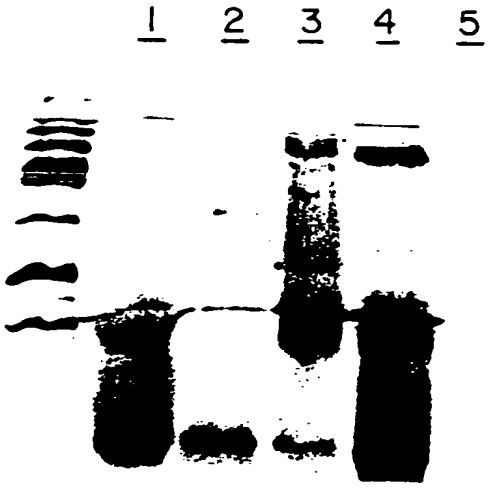


FIG.23B

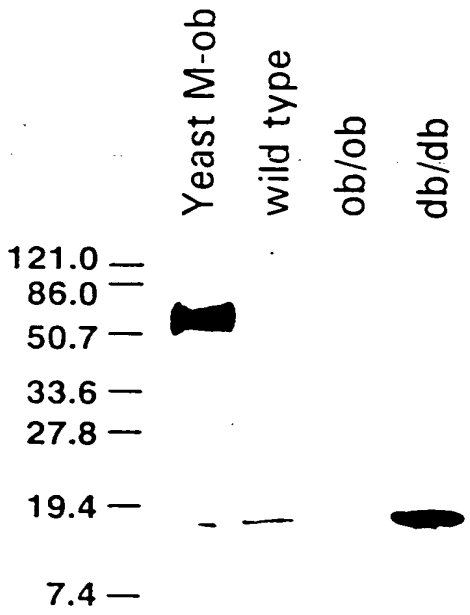


FIG.24A

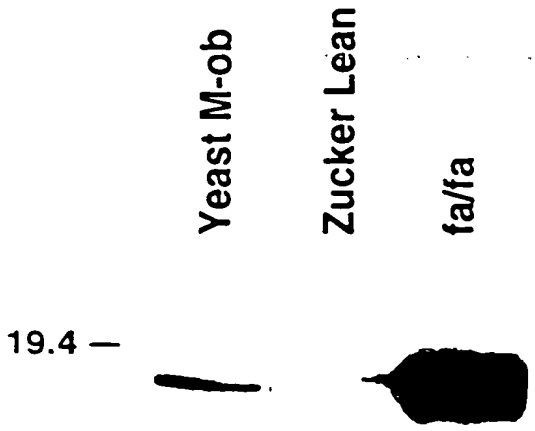


FIG.24B

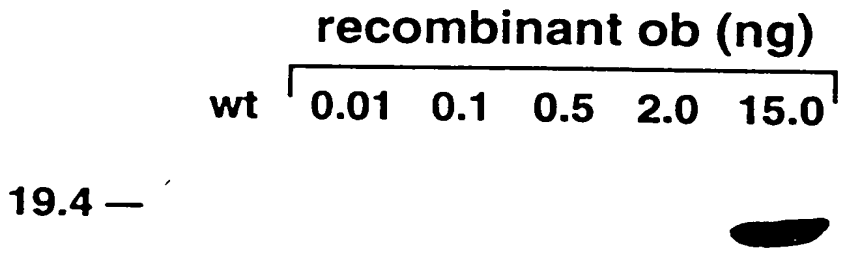


FIG.24C

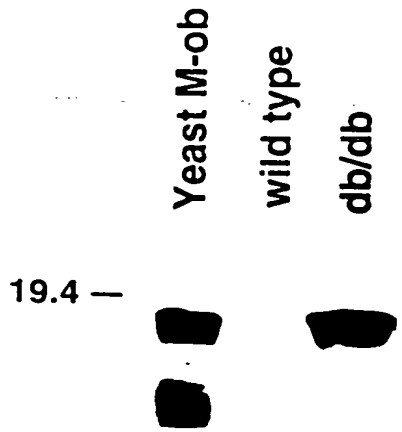


FIG.24D

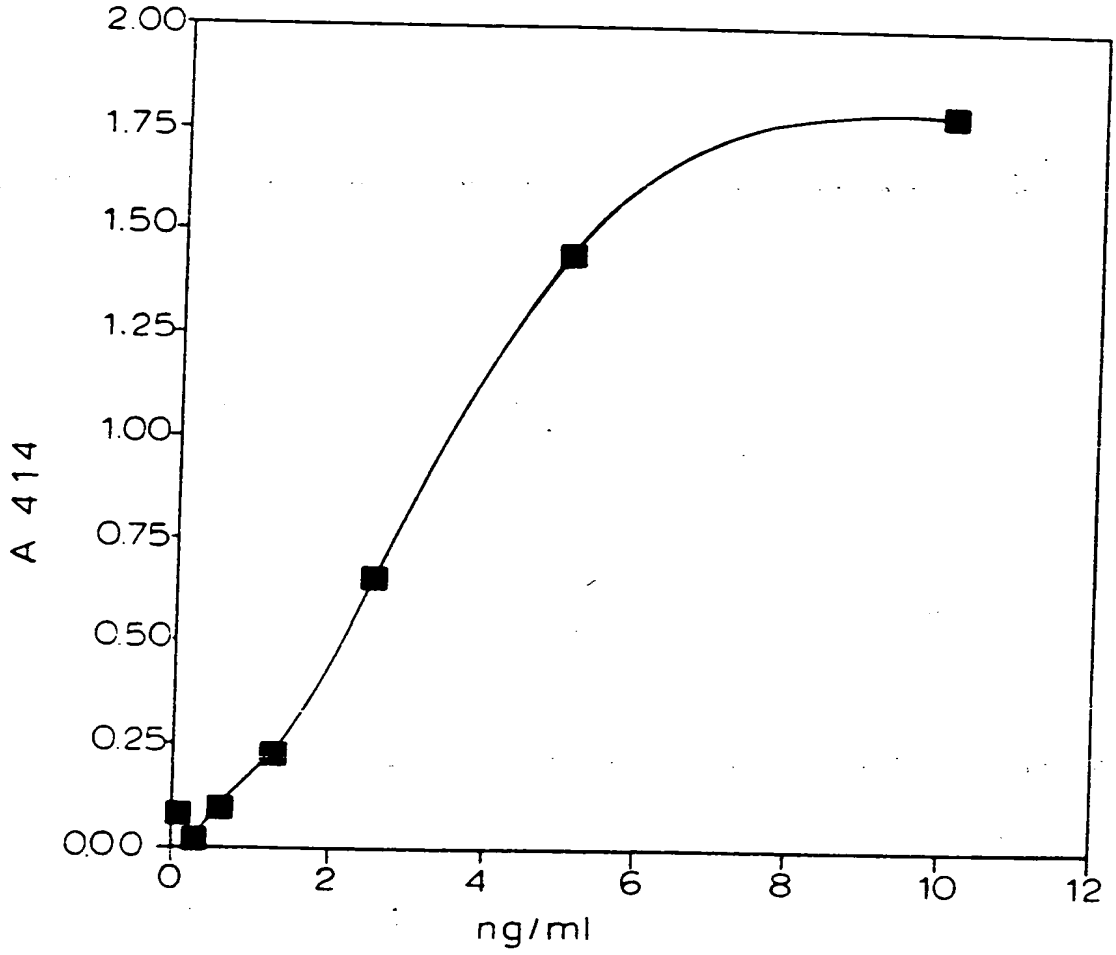


FIG.25B

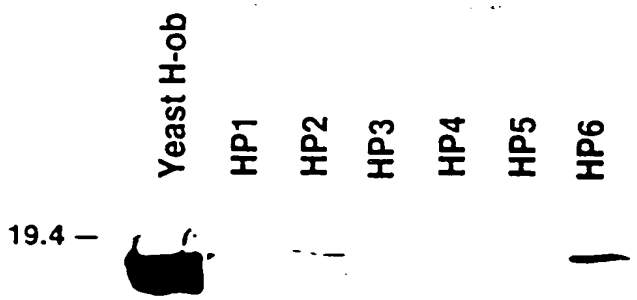


FIG.25A

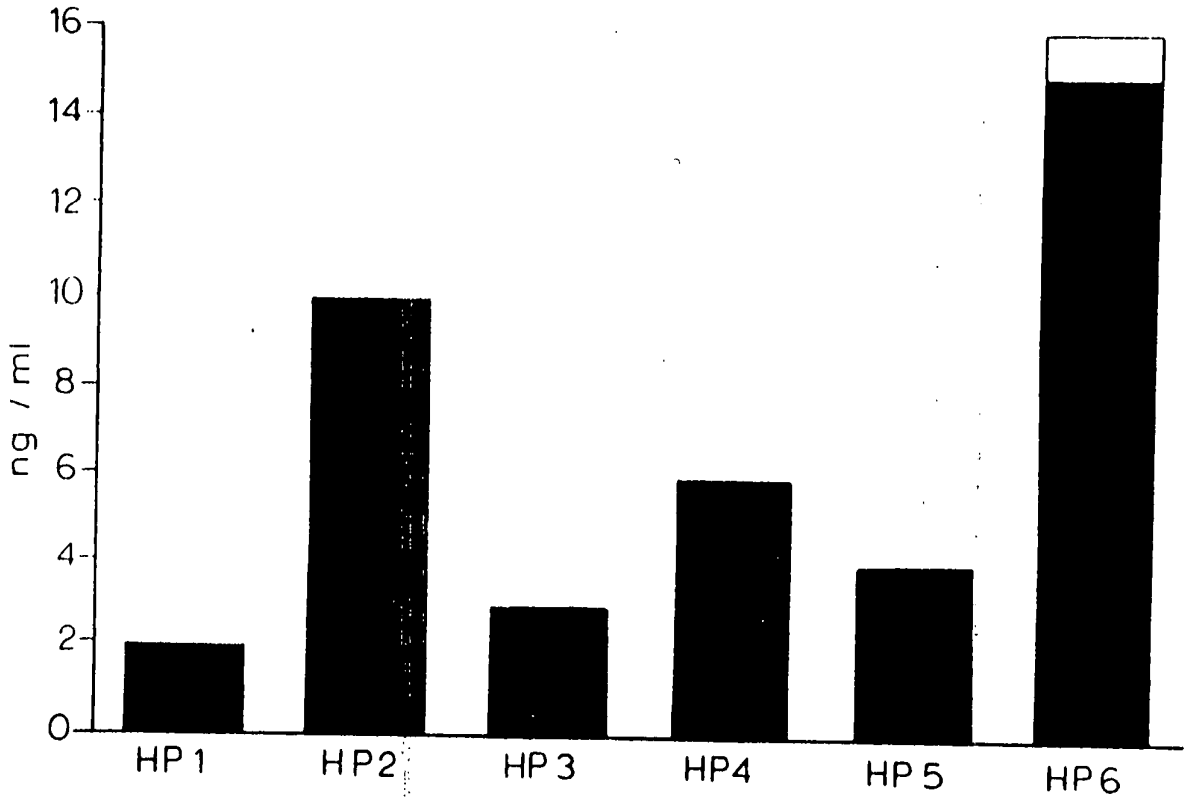


FIG.25C

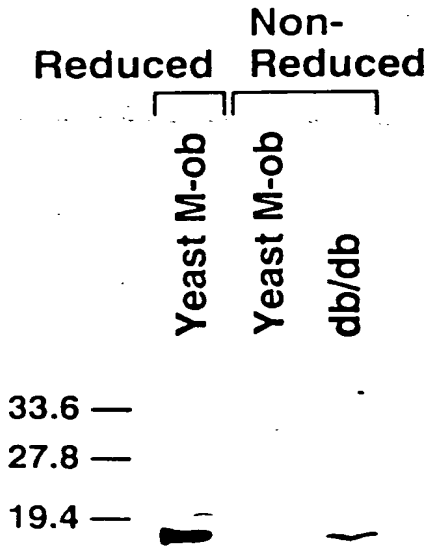
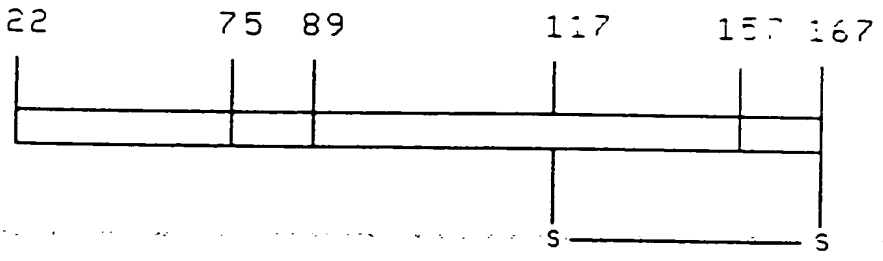


FIG.26A

Human ob



Peptide	Mass(Da)	
	Expected	Observed
22-167	16,024	16,024 ± 3
22-75	5936.9	5936.6 ± 1
76-89	1562.7	N.D.
90-167	8434.5	8435.6 ± 1
158-167	1131.9	N.D.

FIG. 26 B

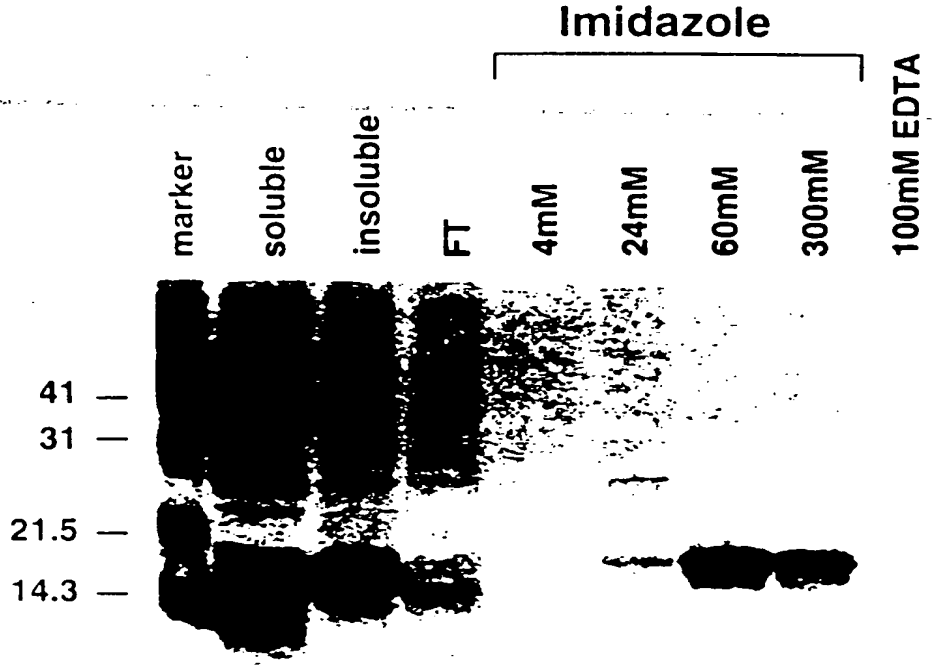

Imidazole
marker
soluble
insoluble
FT
4mM
24mM
60mM
300mM
100mM EDTA
41
31
21.5
14.3

FIG.27

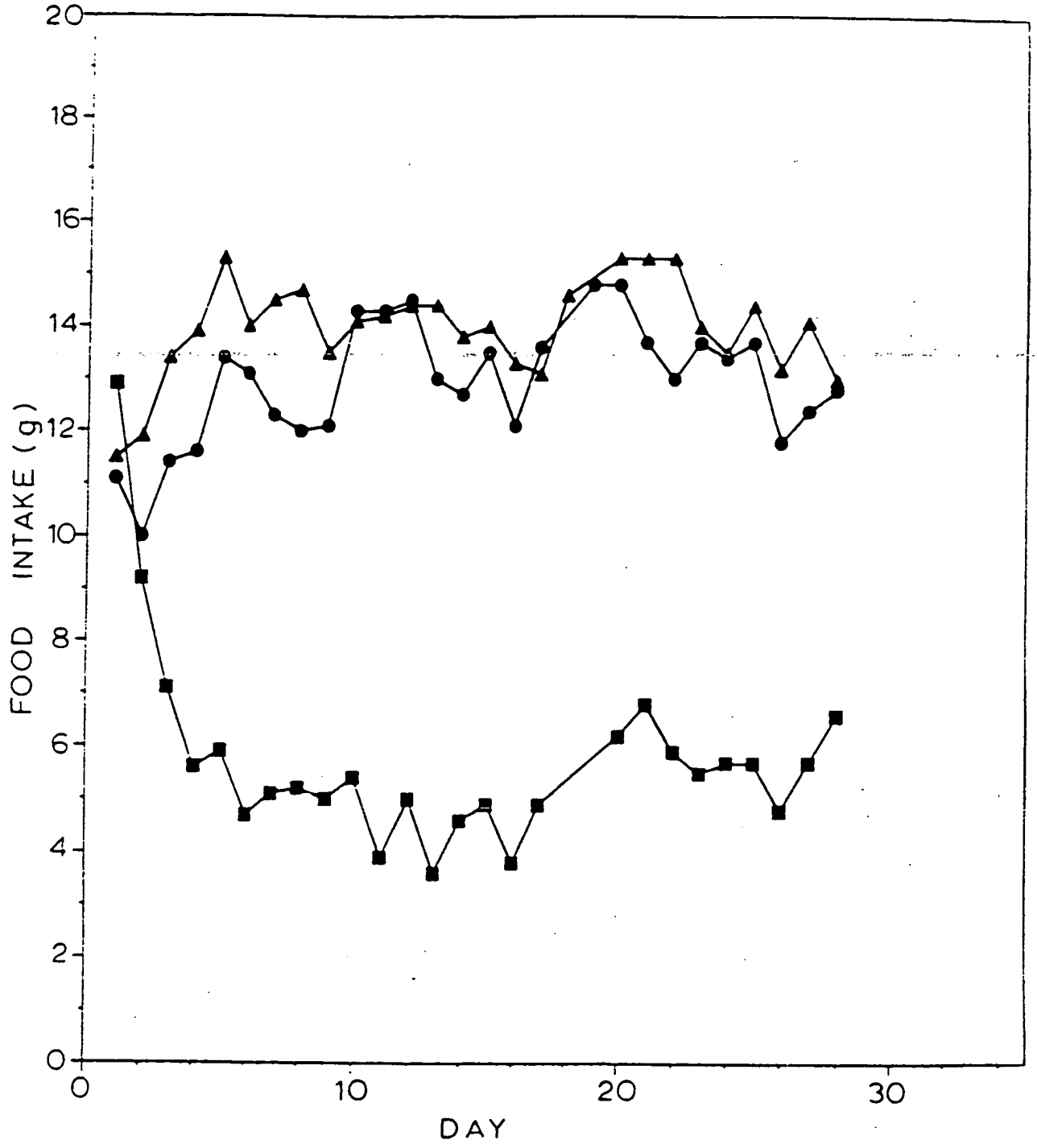


FIG.28A

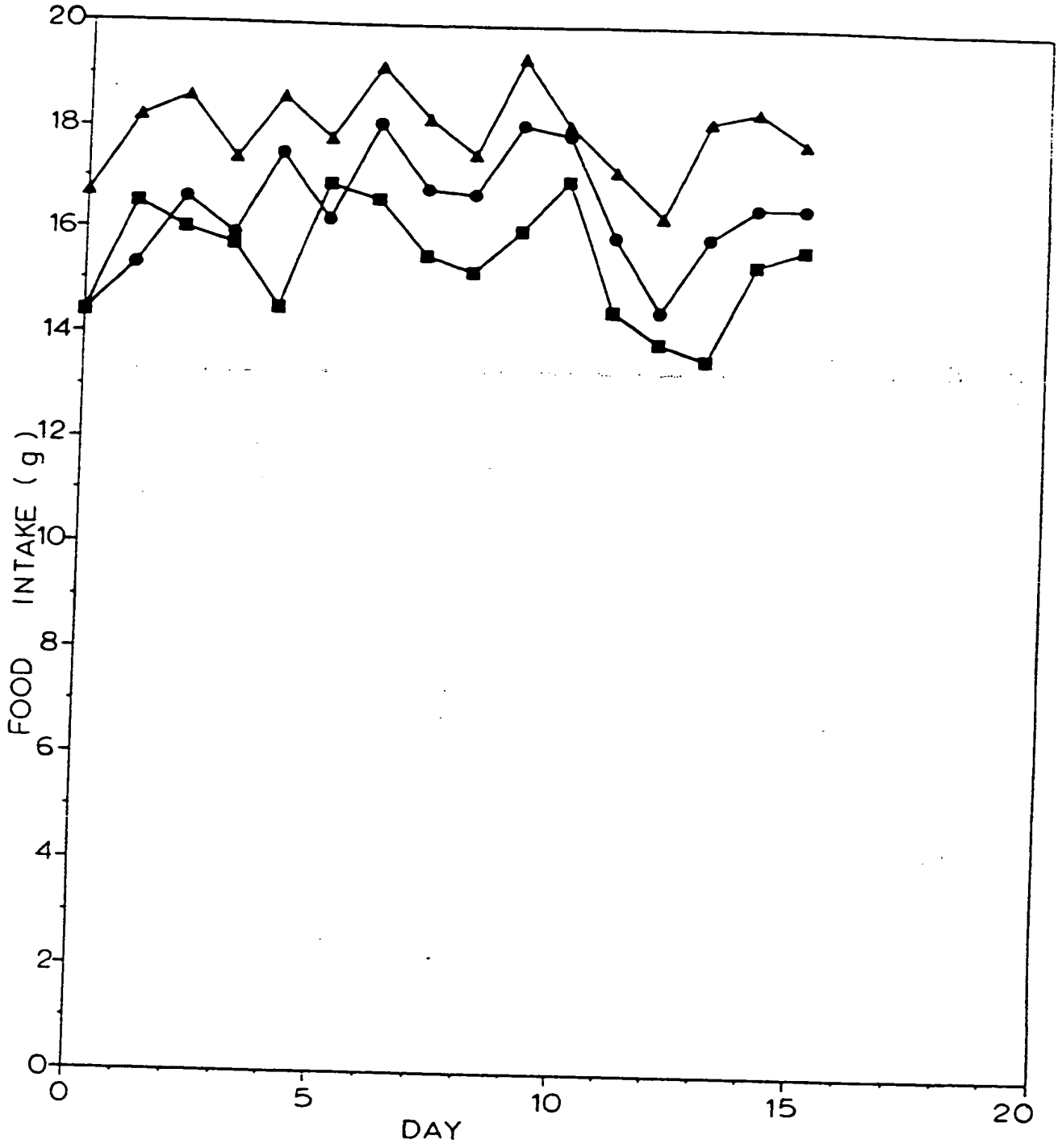


FIG.28B

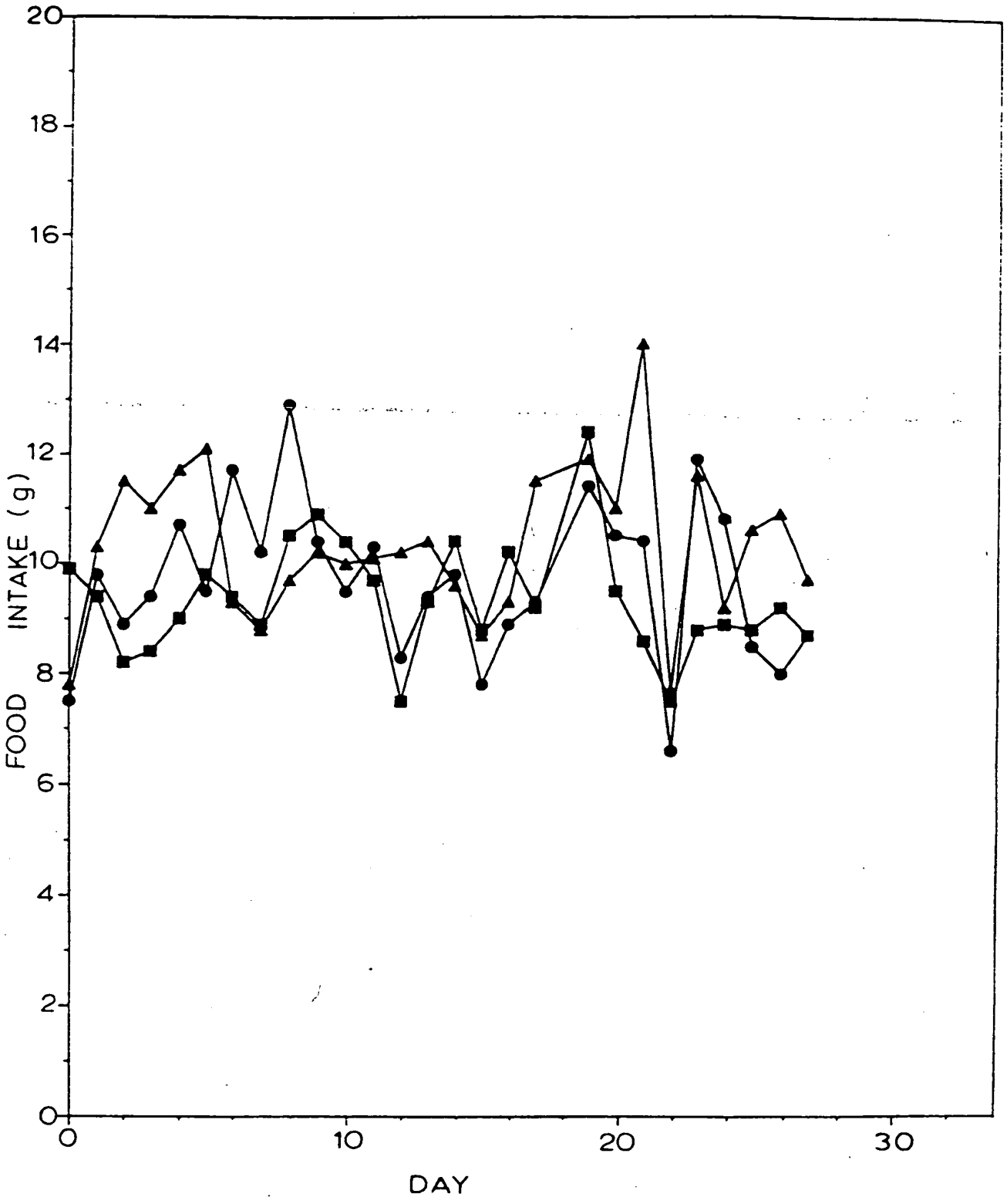


FIG.28C

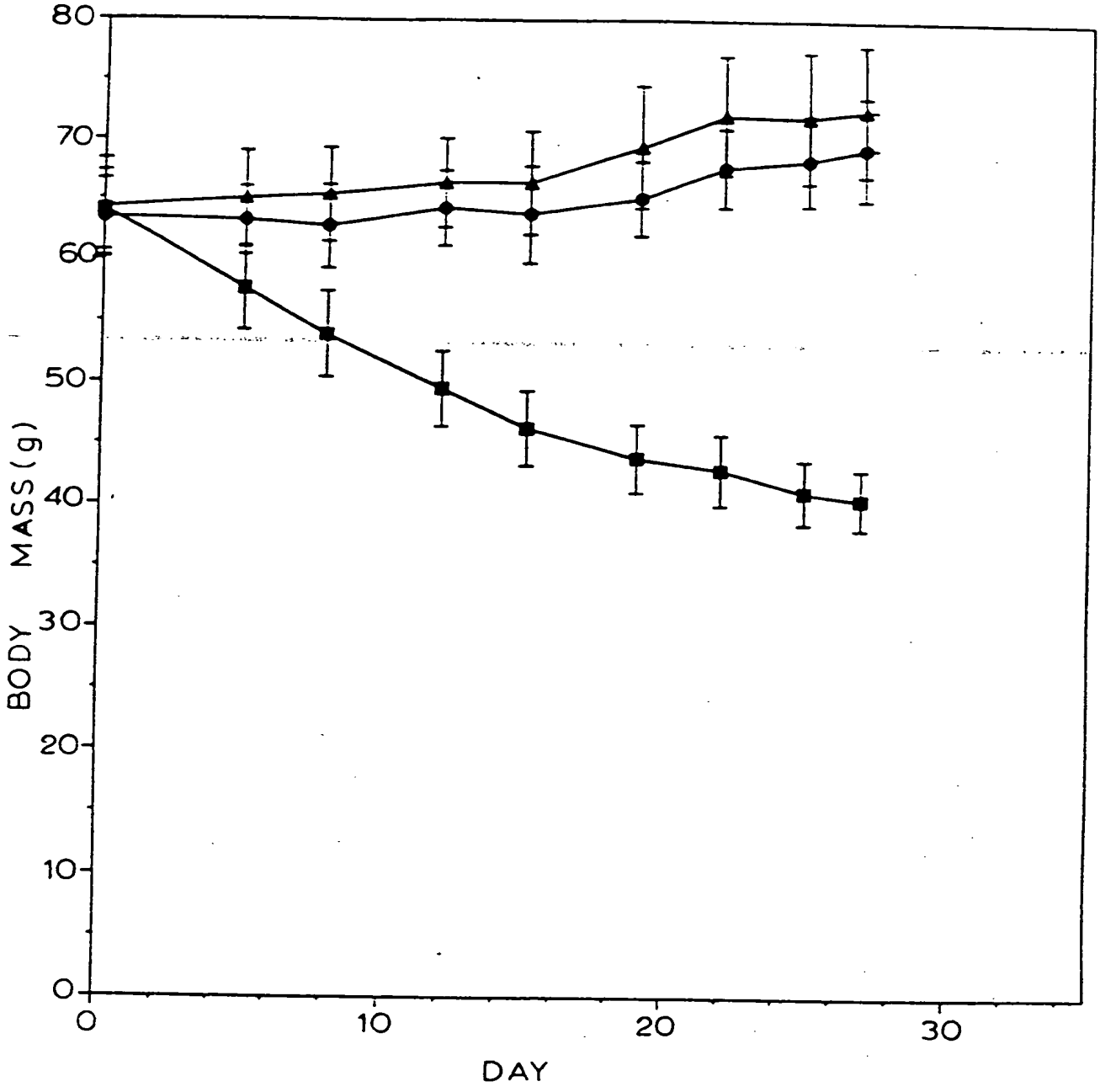


FIG.28D

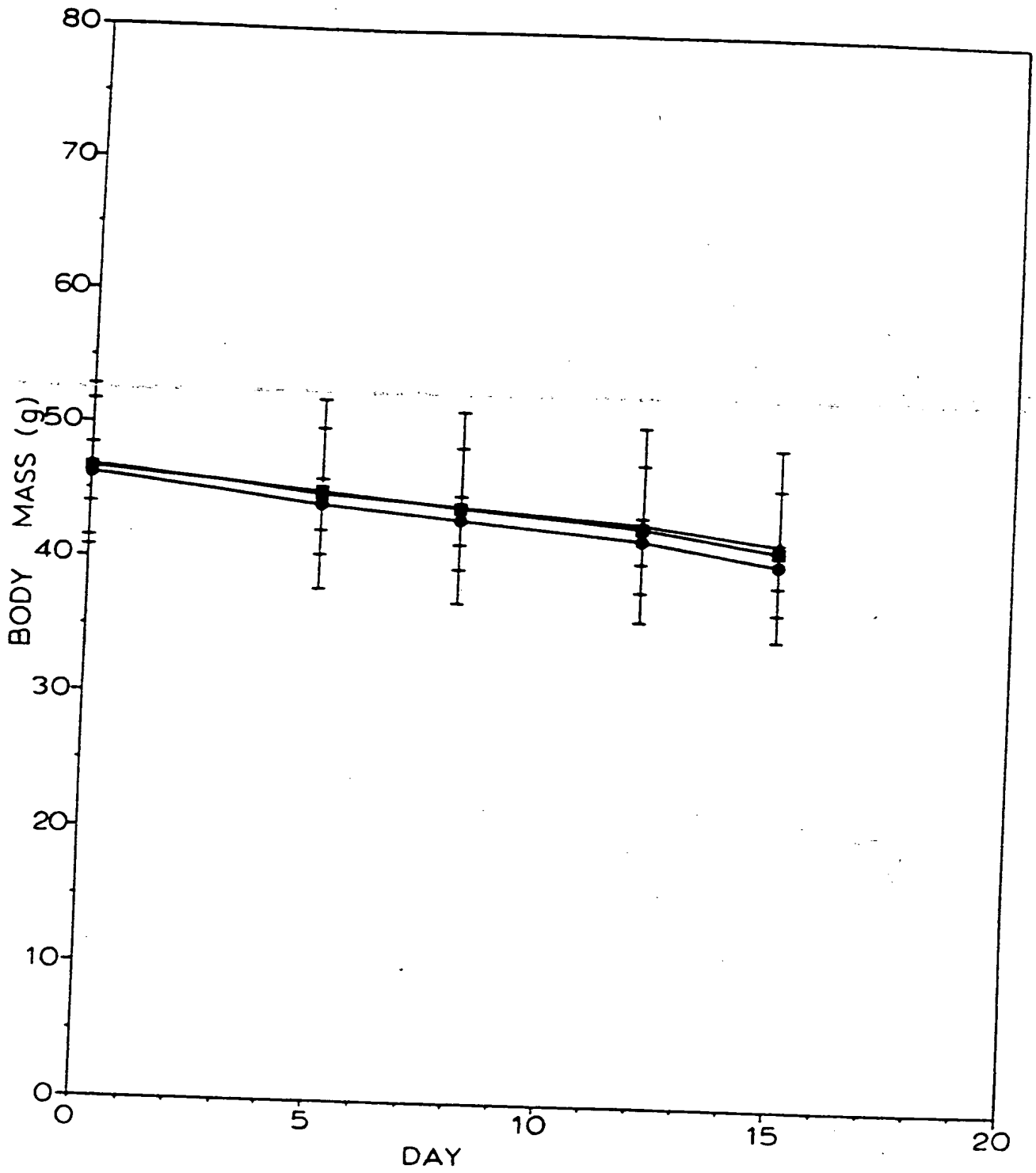


FIG.28E

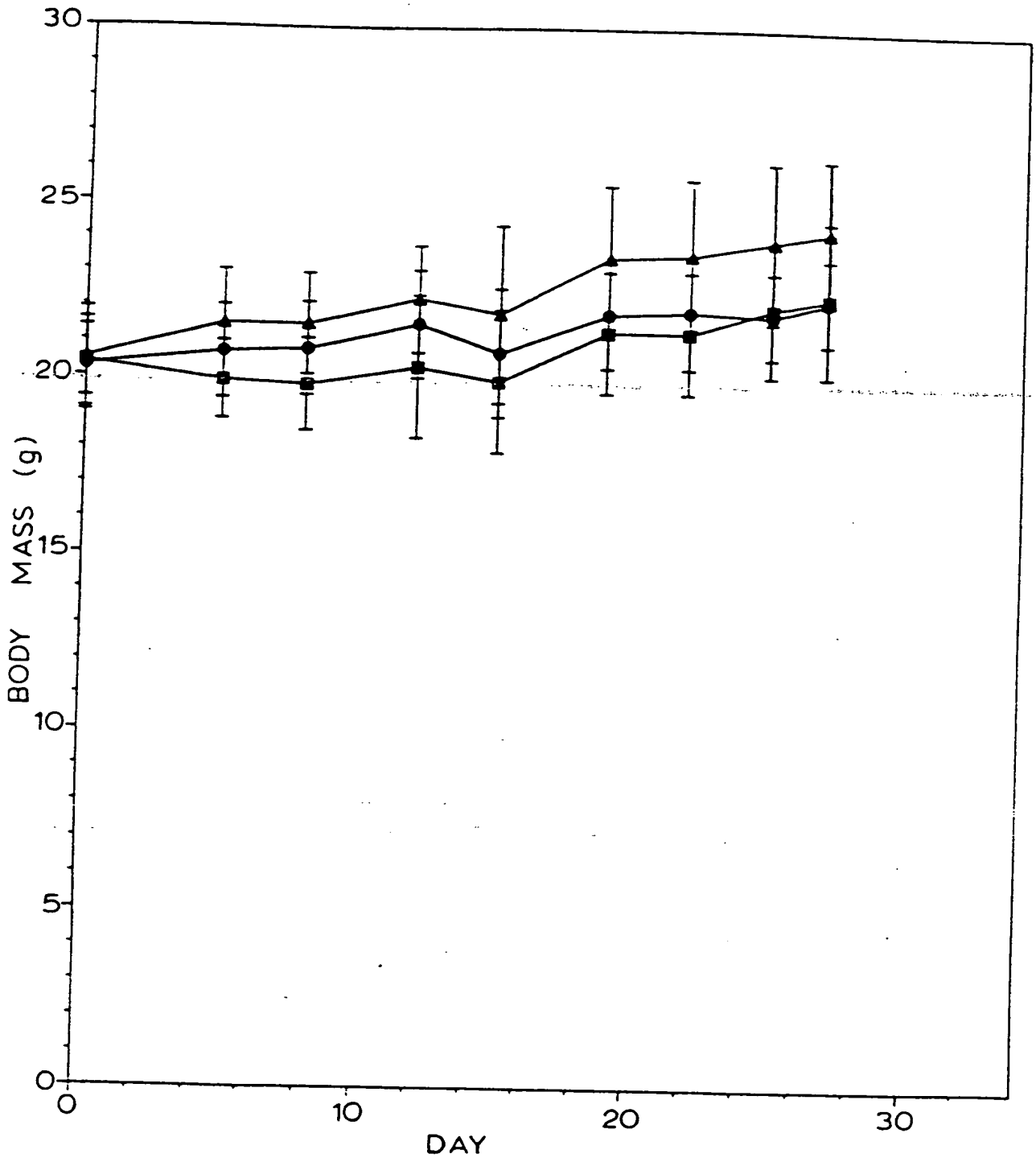


FIG.28F

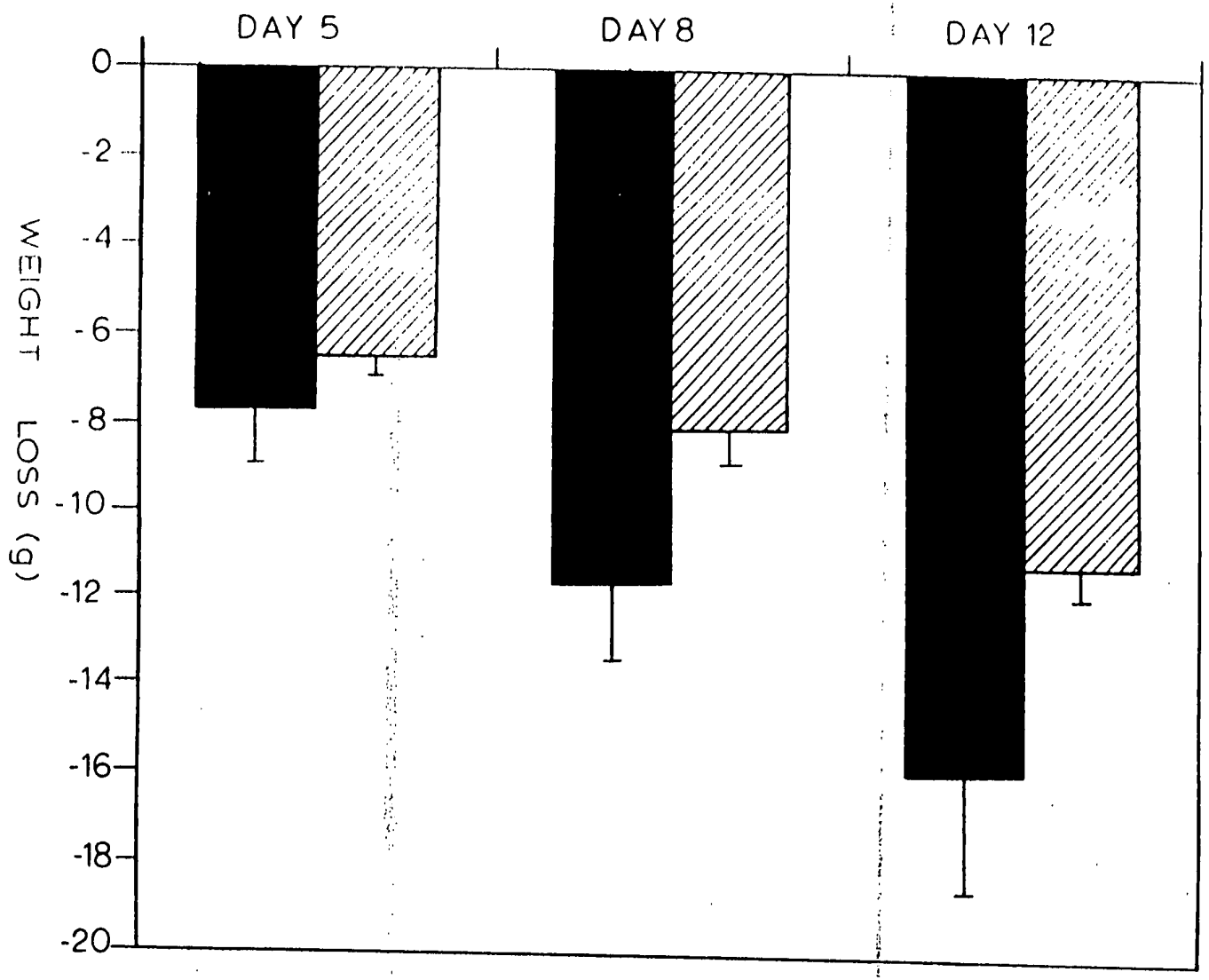


FIG.29A

FIG.29B

FIG.29C

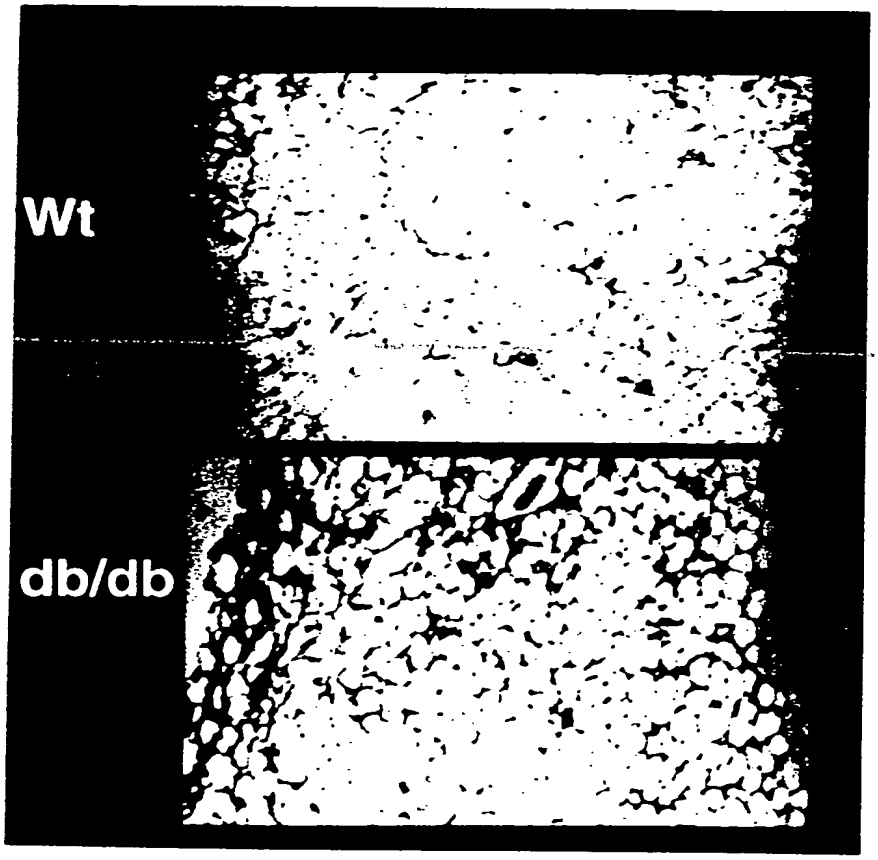


FIG.30

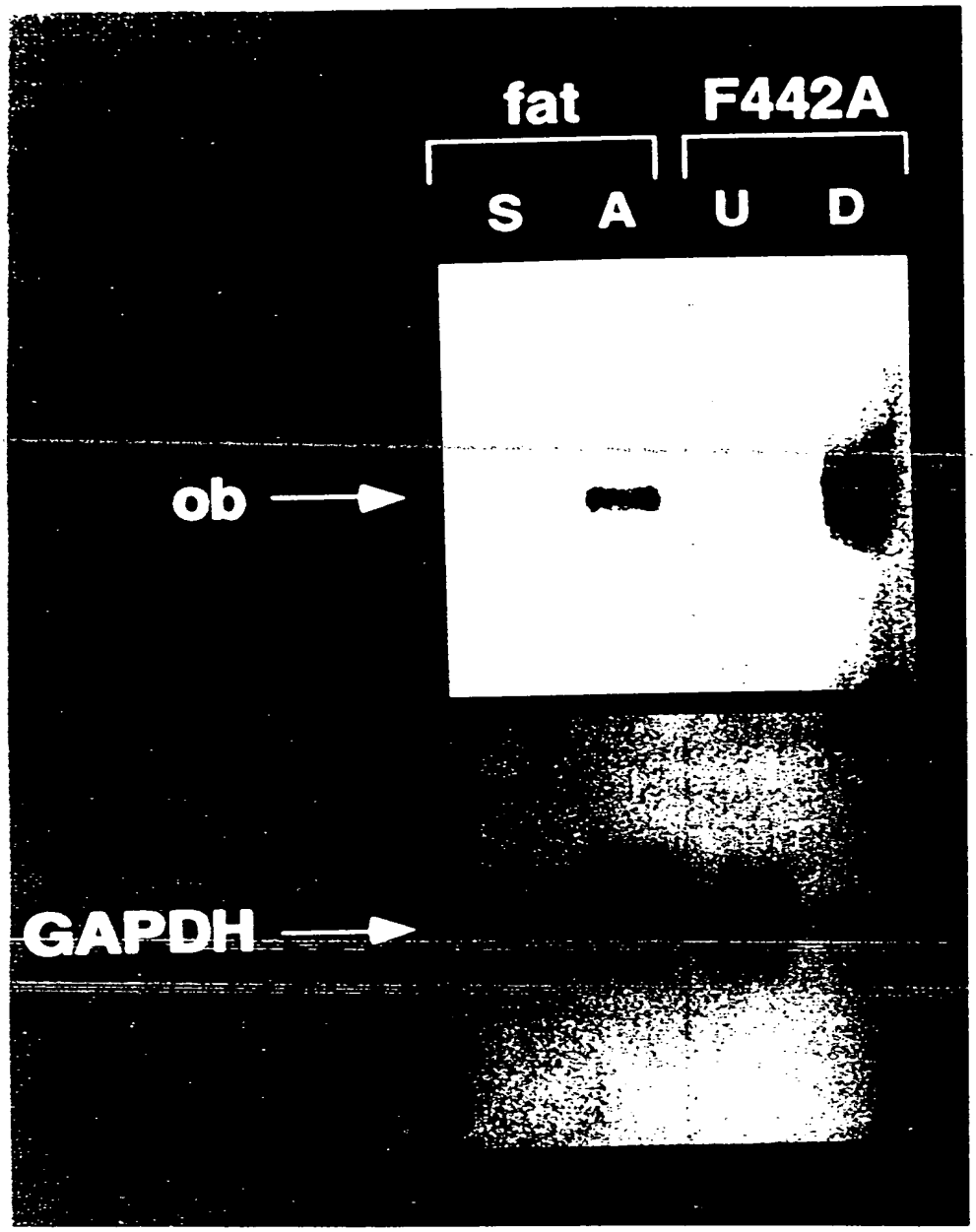


FIG.31

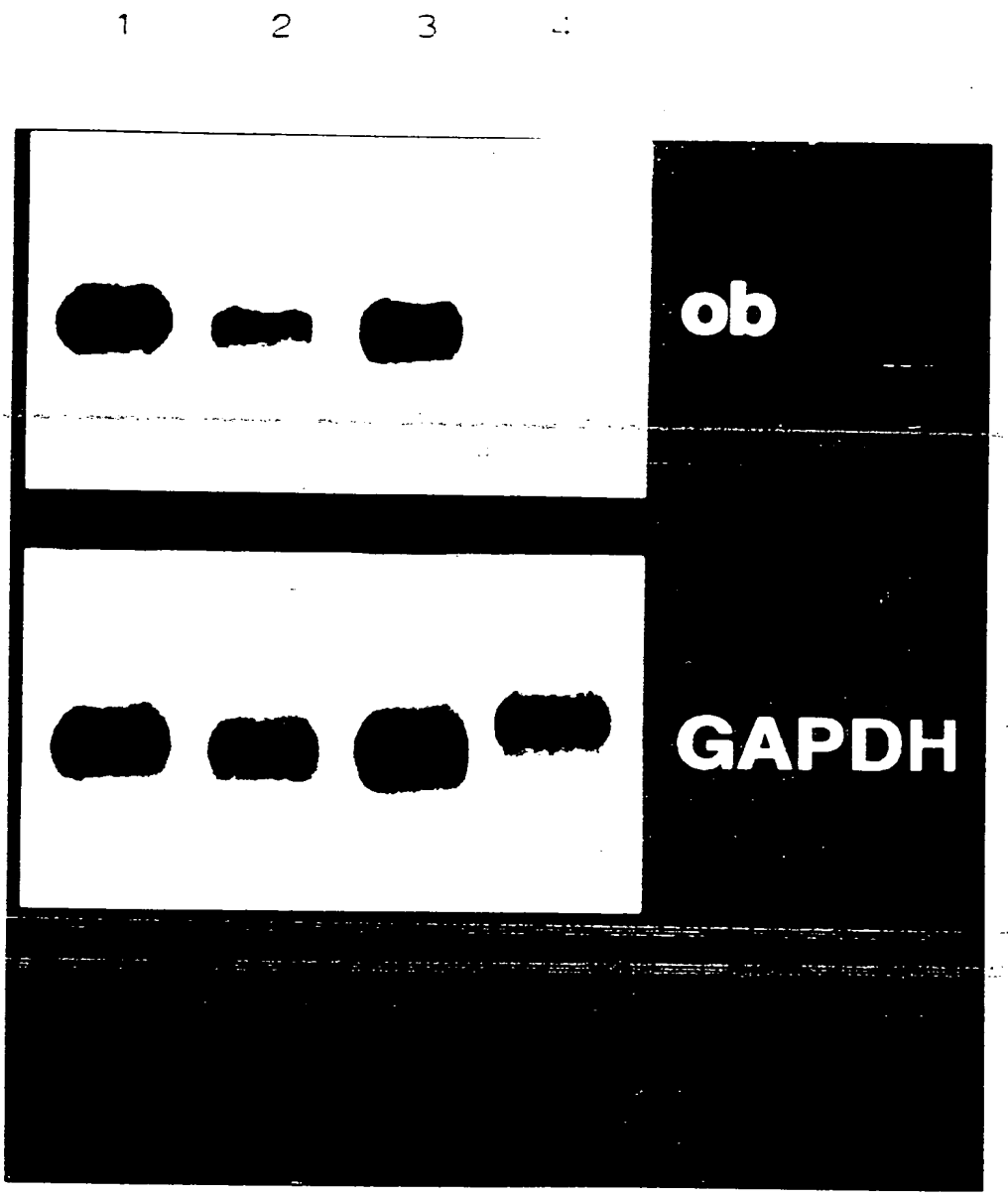


FIG.32A

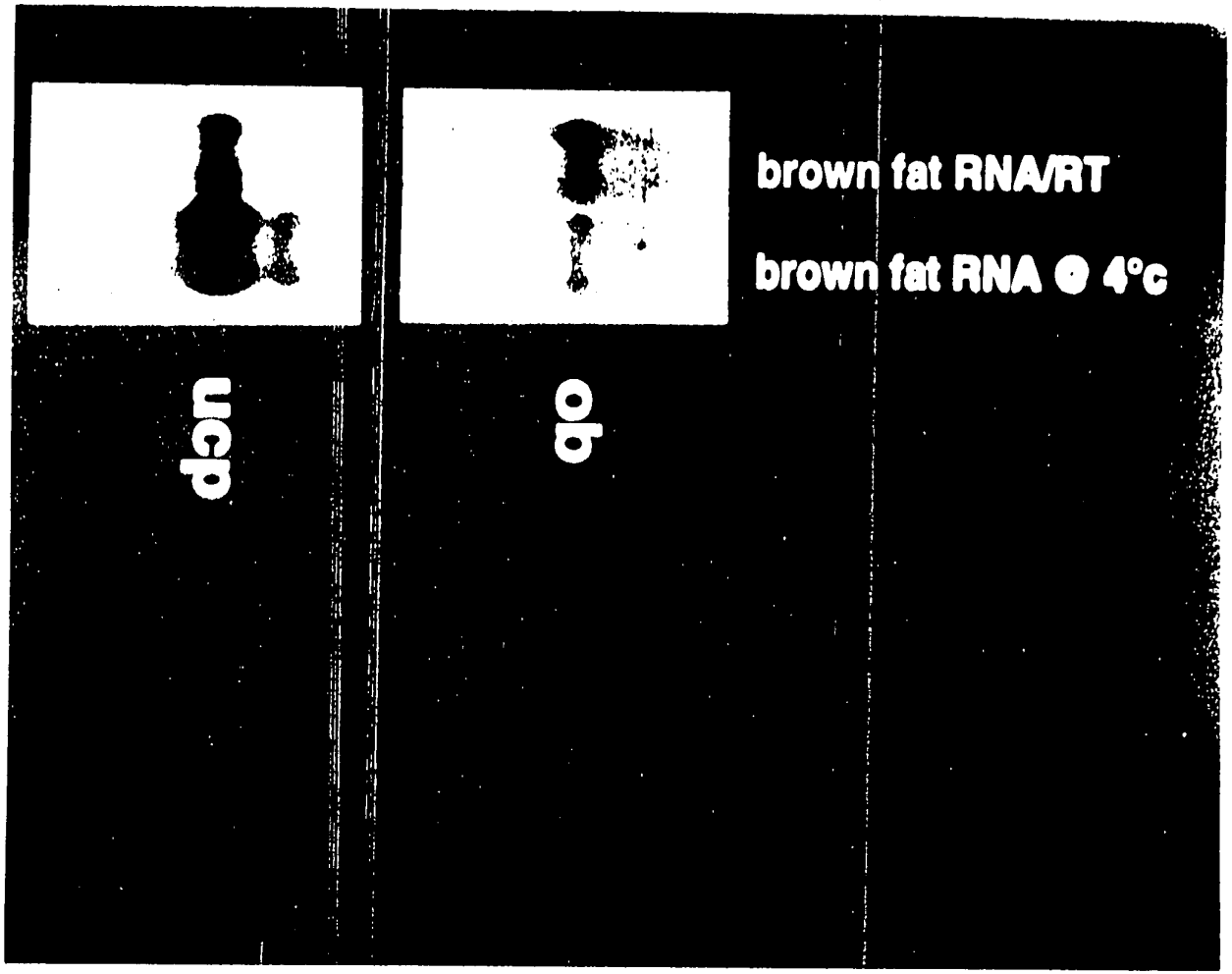


FIG.32B

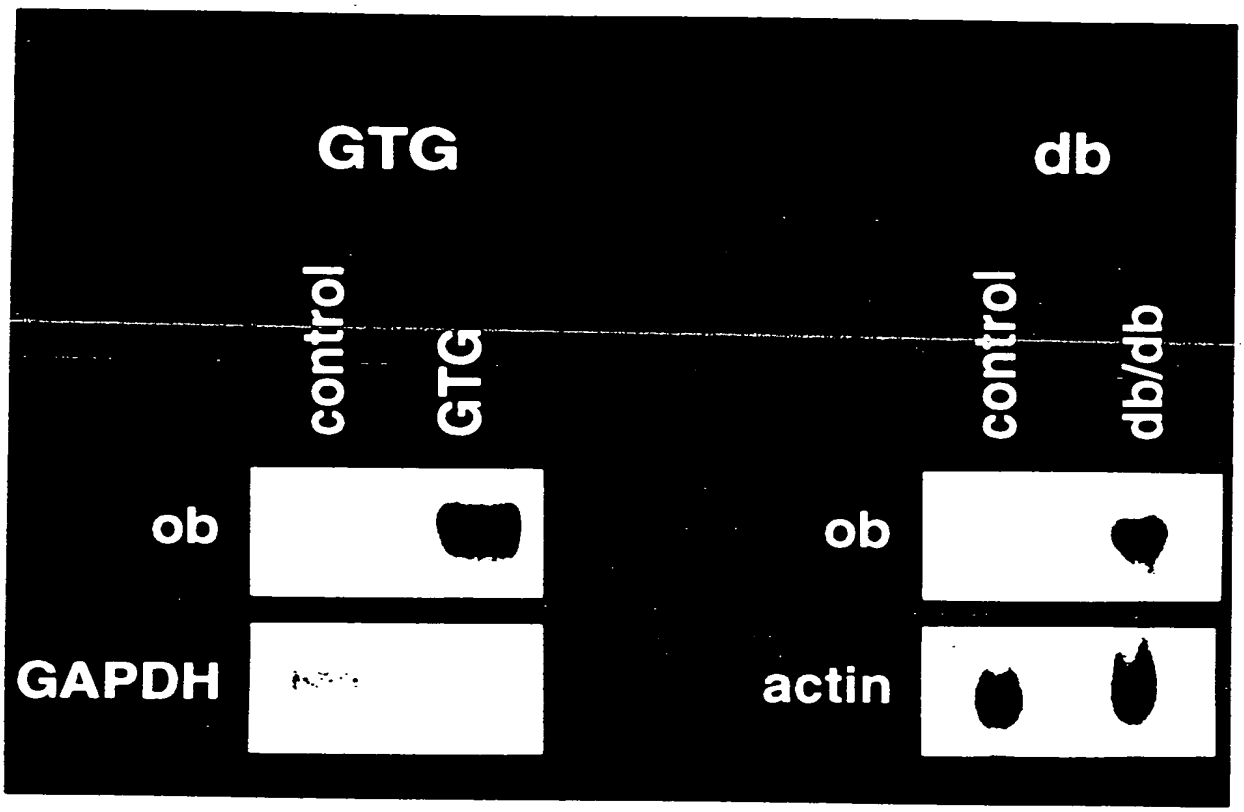


FIG.33

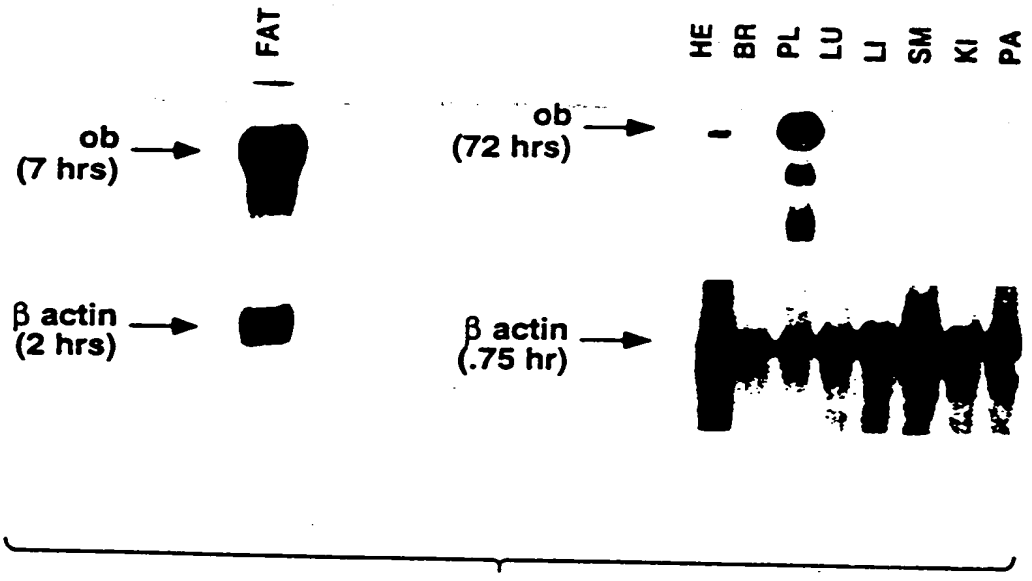

FAT
HE
BR
PL
LU
LI
SM
KI
PA
ob
(7 hrs)
β actin
(2 hrs)
ob
(72 hrs)
β actin
(.75 hr)

FIG.34

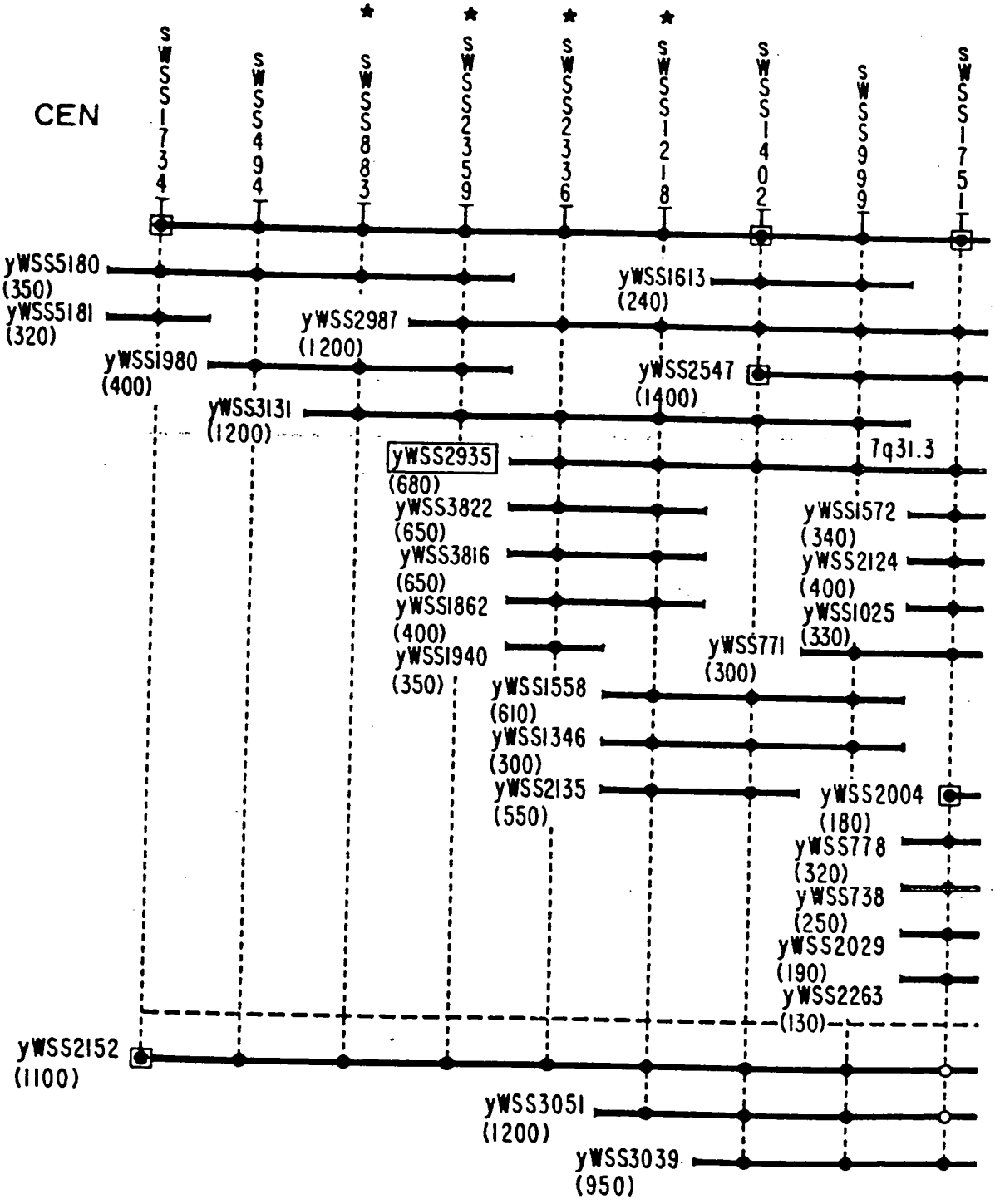

CEN
SWSS1734
SWSS494
SWSS883
SWSS2359
SWSS2336
SWSS1218
SWSS1402
SWSS999
SWSS1751
yWSS5180
(350)
yWSS5181
(320)
yWSS1980
(400)
yWSS3131
(1200)
yWSS2987
(1200)
yWSS1613
(240)
yWSS2547
(1400)
7q31.3
yWSS2935
(680)
yWSS3822
(650)
yWSS3816
(650)
yWSS1862
(400)
yWSS1940
(350)
yWSS1572
(340)
yWSS2124
(400)
yWSS1025
(330)
yWSS771
(300)
yWSS1558
(610)
yWSS1346
(300)
yWSS2135
(550)
yWSS2004
(180)
yWSS778
(320)
yWSS738
(250)
yWSS2029
(190)
yWSS2263
(130)
yWSS2152
(1100)
yWSS3051
(1200)
yWSS3039
(950)

FIG. 35A

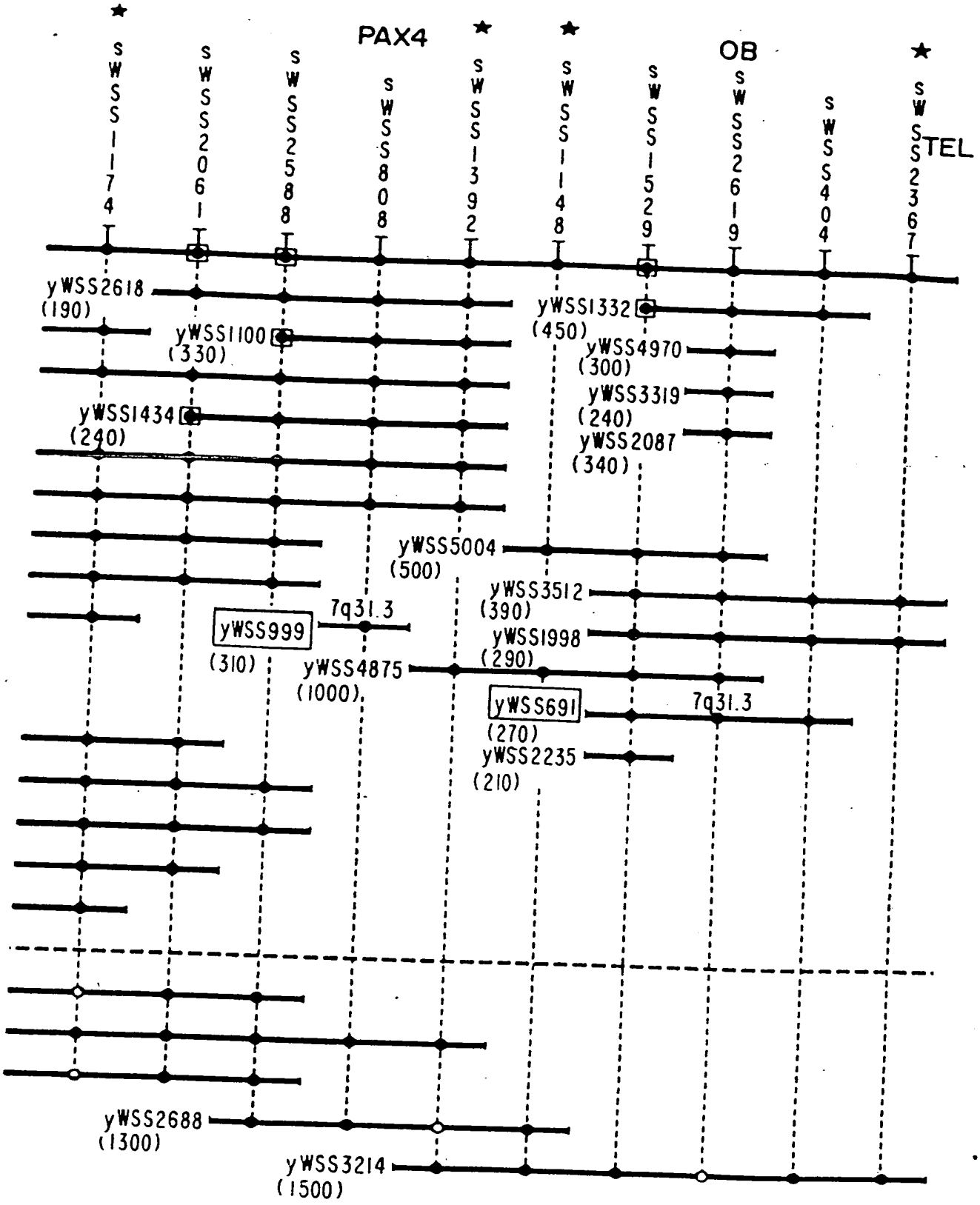

PAX4
OB
TEL
sWSS1174
sWSS2061
sWSS2588
sWSS808
sWSS1392
sWSS148
sWSS1529
sWSS2619
sWSS404
sWSS2367
yWSS2618
(190)
yWSS1100
(330)
yWSS1434
(240)
yWSS1332
(450)
yWSS4970
(300)
yWSS3319
(240)
yWSS2087
(340)
yWSS5004
(500)
yWSS3512
(390)
yWSS1998
(290)
yWSS999
(310)
7q31.3
yWSS4875
(1000)
yWSS691
(270)
7q31.3
yWSS2235
(210)
yWSS2688
(1300)
yWSS3214
(1500)

FIG. 35B